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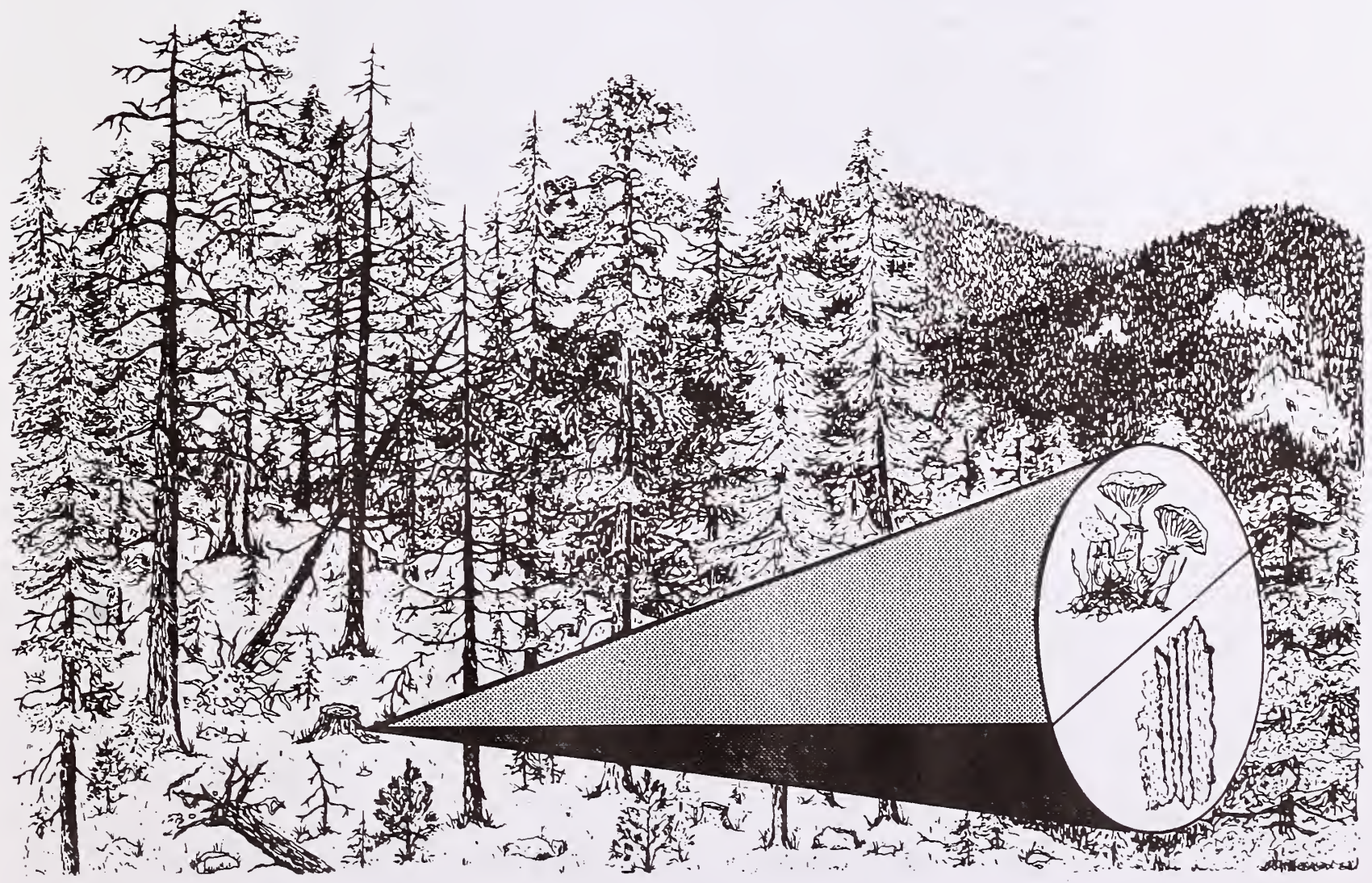
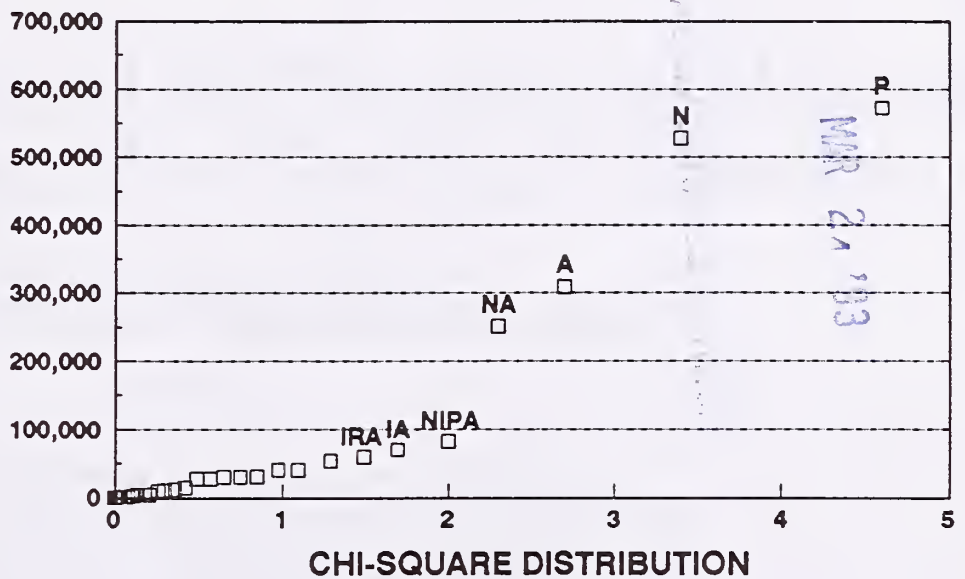
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Sensitivity Analyses of the Western Root Disease Model to User-specified Starting Parameters

Michael A. Marsden

SUM OF SQUARES



Abstract

Tests of the Western Root Disease Model identify the user-supplied parameters to which the model is most sensitive. A series of simulation runs are arranged as a designed experiment. Analysis of variance is used to identify significant starting conditions based on attributes of the stand simulations. Probability plots of the sum of squares associated with the model parameters are used to rank effects. This gives the user a reference for the relative effect of each parameter. Short-term model simulations without the harvest of trees are sensitive to such parameters as the proportion of trees infected and the proportion of root systems colonized. Long-term simulations are more sensitive to such parameters as initial area infected and number of disease centers. Model simulations with harvest are sensitive to the removal of stumps and the planting of resistant species.

Sensitivity Analyses of the Western Root Disease Model to User-specified Starting Parameters

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INTRODUCTION

The Western Root Disease Model is designed to predict the spread and impact of pathogenic *Armillaria* spp. or *Phellinus weirii* (Murr.) Gilbn. in conifer stands in the Western United States (Stage et al. 1990). The model is linked to the Prognosis Model for Stand Development (Wykoff 1986, Wykoff et al. 1982).

This paper presents the sensitivity analyses of two base sets of user-controlled parameters for the Western Root Disease Model. These analyses include ranking the model parameters in terms of their effect on the simulation of future stand conditions. The statistical methods used in these analyses are also presented.

Sensitivity analysis is a part of the model development process. The analyses presented here are a part of a series of such analyses that have led to the discovery and correction of several errors and omissions in the model. The Western Root Disease Model release 1 as linked to the North Idaho variant of the Prognosis Model for Stand Development release 6.0 was used in the simulations.

In the development of the Western Root Disease Model some test runs of the model were made. These were arranged in a factorial design. No statistical analyses of the results were computed. Means were compared for starting conditions one factor at a time.² In this paper the use of a factorial design is expanded upon, and statistical analyses are used. Two statistical methods used in evaluating the results are the analysis of variance and the probability plotting of squared contrasts. An example of the use of a factorial design in the sensitivity analysis of a simulation model is given in Box et al. (1978). The use of probability plots is further expanded upon in Gnanadesikan (1977).

CONDITIONS FOR TESTING

In the sensitivity tests for this report the two diseases, caused by *Armillaria* or *Phellinus*, are treated separately. The testing is further divided. The simulation of stands following inventory but without harvest is presented first. There is a basic set of five parameters for the starting disease conditions of the stand to be simulated. This report ranks these parameters with respect to several attributes of the simulated stand. The stand tree data may contain information to set starting disease conditions.

² McNamee, P.J.; Webb, T.M.; Everitt, R.R.; Greit, L.A. 1985. Final report of a project to construct a prototype root disease model for silvicultural planning in the western United States. Unpublished report. Moscow, ID: U.S. Department of Agriculture, Forestry Sciences Laboratory. 104 p.

McNamee, P.J.; Sutherland, G.D. 1986. Root disease model sensitivity analysis. Draft unpublished report. Moscow, ID: U.S. Department of Agriculture, Forestry Sciences Laboratory. 308 p.

The simulation of stands following inventory with a harvest and a regeneration of a new stand is presented second. In this case we are interested in the carryover of the root disease into the new stand. A second set of parameters for the carryover conditions is examined. These basic parameters that control the disease status during the carryover process are ranked with respect to effects on several stand attributes.

BASIC MODEL

Model Overview

User control of the Western Root Disease Model as linked to the Prognosis Model for Stand Development is through a KEYWORD system. For a complete guide to the model and its use, refer to the user's guide (Stage et al. 1990). Only the basic set of KEYWORDS and their parameters will be discussed here.

A subset of KEYWORDS to run this model would be RRIN, RRTYPE, RRINIT, SAREA, RSEED, SPREAD, and END. RRIN calls the Western Root Disease Model. This is required by the Prognosis Model if root disease is to be simulated in addition to the stand simulation. RRTYPE determines if *Armillaria* or *Phellinus* root disease is to be simulated. RRINIT specifies most of the initial stand conditions with respect to root disease. SAREA specifies the total stand area. RSEED specifies a starting value for the random number generator within the model. SPREAD specifies if the simulation of the spread of root disease will be static, a constant rate, or dynamic, based on tree density and location. Dynamic spread will be used in all tests for this report. END indicates the last of the keywords for the Western Root Disease Model.

RRTYPE has one parameter field associated with it. The field value is 1 if *Armillaria* is to be simulated. The field value is 2 when *Phellinus* is to be simulated.

RRINIT has six parameter fields associated with it. The first field indicates whether the distribution of root disease within the stand is random or fixed. Only random distribution will be addressed here. For a discussion of the fixed and random distribution of root disease see Marsden (1992). The second parameter field determines the number of root disease centers within the stand. The third and fourth fields determine the ratio of infected trees to noninfected trees within the root disease centers. The fifth field specifies the proportion of the root system that is colonized for an average infected tree. The sixth field specifies the total infected area (acres) in the stand.

Because the area infected is specified on the RRINIT keyword, the total stand area must also be specified. This is done on the single field on the SAREA keyword.

RSEED's only field is a starting number. This value controls the random location of root disease centers within the stand. It also affects the location of trees within a model's representation of the infected area. The significance of this value will be seen later.

A set of KEYWORDS for a simulation of one of the test stands is given in table 1. For evaluation, the basic user information will be referred to as five parameters:

- N, number of centers;
- I, proportion of trees infected;
- P, proportion of root system colonized;
- A, area infected; and
- R, replication.

This set of parameters will be evaluated first for *Armillaria* and then for *Phellinus*.

Design of Tests

In the design of this experiment, two values are selected for each parameter. For 5 parameters this results in 32 combinations of parameter values. Four stands are selected for simulation tests. The complete experiment is then 128 simulation runs of the Western Root Disease Model. The stands selected were from Crow Creek on the Lolo National Forest, Idaho. These stands were chosen to demonstrate our use of the Western Root Disease Model; they were not selected at random. A description of these stands is given in Appendix A. For this experiment, each stand is modeled as an area of 23 acres.

The Western Root Disease Model represents a stand area, regardless of shape, as a square of the same size as the stand area. Within this square, root disease centers are modeled as circles. The user can specify based on inventory data the number of centers and the total area infected. The model's representation of a stand of 23 acres in size with 2 root disease centers and a total infected area of 2 acres is given in figure 1. This same stand with 10 centers and the same total area infected is shown in figure 2. The model located the centers at random, subject to the restriction that there is little overlap of the centers. Overlap would reduce the total area infected. There is a model option that allows the user to specify the location and size of each center. That option is intended for the simulation of test areas with intensive inventory data (Marsden 1992).

Values assigned to each parameter in this analysis represent large differences in disease conditions. The range of values selected for parameters can greatly affect the analysis. The choices used here are based on the model limitations and past experience with testing the model. A model limitation, for example, is the proportion of root system colonized, P, which can vary only from 0 to 1. Mortality in most host species occurs with 0.75 of the root system colonized. One previous experience in testing the model concerns the initial number of root disease centers. Past tests have shown the model to be more sensitive to values between 1 and 10 than between 10 and 100 for the number of initial centers.

The first parameter, N, is the number of disease centers in the stand and it is set to 2 or 10. The second parameter, I, is the proportion of trees in an infection center that are

infected. This is set to .05 or .25 by specifying the number of trees per acre in each infection class. The third parameter, P, proportion of the root system colonized, is set to 0.20 or 0.60. The proportion of the root system colonized when root disease will kill the tree varies by tree species and by root disease type. Area infected, A, is set to 2 acres or 4 acres. This range is limited because the total stand size specified is only 23 acres. Setting larger initial acres of infection leads to the infection spreading well beyond the boundary of the stand before long time periods can be simulated. And replication, R, is set to one of two different random starting values: 28413 or 3941. Since the locations of root disease centers in the stands are modeled as random, R determines two different sets of center locations.

Several other operations in the root disease model are stochastic and affected by changing the random start. For example, when the root systems of two trees are simulated to overlap, infection can be transferred from one to the other. Changing the random start can change the pattern of spread. Because trees are modeled with a probability of infection, stochastic spread of the disease results. Such changes are believed to be small compared to the initial location of centers and trees by the model.

The stand simulations are run for 10 cycles. Each cycle is 10 years in length. The Prognosis Model writes summary tables of stand conditions at the end of each cycle. The Western Root Disease Model writes summary tables for the conditions within the infected area of the stand at the end of each cycle. The area infected itself is subject to change from cycle to cycle as the disease spreads throughout the stand. Any of the items reported on the two summaries could have been used in our analysis. Here we will present only a few root disease model summary values.

Analyses for *Armillaria*

First-Cycle Tree Mortality

The initial criterion selected from the root disease summary is the tree mortality for the first cycle, DMORT93. DMORT93 is the tree mortality (trees per acre) only within the disease area. The first cycle ends in 1993. The analysis of variance for the mortality rate for the first 10-year cycle is given in table 2. Here we used the variation among stands and all its interaction terms as our pooled error term. The Western Root Disease Model contains several stochastic elements. A change in the starting value for the random number generator within the model will result in a change in the stand simulation. Using the variation among stands as our error term allows the user-controlled starting value to be treated as just another model parameter. All other effects, along with factors in the design (except stands), are fixed.

The simulation of tree mortality for the first 10-year cycle is sensitive to our changes in the initial proportion of trees infected and to the proportion of root systems colonized. Of less statistical significance, alpha = 0.10 level, is the change in the number of centers, N, and the change in the random start, R, as represented in interaction term NR in the analysis of variance (table 2).

For this analysis we wish to rank the effects of the parameters with respect to one another. Such ranking is more important for the parameters that have the largest effects on the attributes of the simulated stand. Each effect, except the error term, has one degree of freedom associated with it in our design. For ranking effects, the total of the responses for the stands simulated under the same experimental conditions is the basic measurement. Since we have a balanced design we can use the sum of squares from the analysis of variance already computed, ignoring stand effects. The sums of squares associated with these effects in the analysis of variance table are ordered by largest to smallest. There are 31 single-degree-of-freedom sums of squares. After sorting, these form a cumulative empirical distribution with associated probabilities, $(1-1/31)$, $(1-2/31)$, ..., $(1-31/31)$. Under a null hypothesis of no effect, these sums of squares would be distributed as chi-square (Gnanadesikan 1977, p. 137). Each value for the cumulative is solved for the chi-square distribution value for that percentile of a sample. The sums of squares are then plotted against the corresponding values for a chi-square distribution (fig. 3).

Under the null hypothesis, the points should form a straight line. Departure from this trend indicates significant deviation from the hypothesis of no effect. The two points representing factors I and P are greatly separated from the trend indicated by the other 29 points. This agrees with the analysis of variance tests as expected. It also allows us to see the relative effect (squared) not only of the significant effects but of the others as well.

Second-Cycle Tree Mortality

The next criterion selected for analysis is DMORT03, the tree mortality in the second cycle for the root-diseased area of the stand. The second cycle ends in 2003. The analysis of variance is presented in table 3. Here there are seven significant factors. These are the main effects of N, P, A, and the following interactions:

NA, number of centers by area infected;

IA, proportion of trees infected by area infected;

IRA, proportion of trees infected by replication by area infected; and

NIPA, number of centers by proportion of trees infected by proportion of root system infected by area infected.

Parameter I is no longer significant as a main effect but it does occur in three of the significant interactions.

The number of centers, proportion of root system infected, and the area infected are significant in the simulation of tree mortality. Mortality during the first cycle is primarily trees within the centers. For the second cycle the mortality is composed of both trees within the centers and trees on the edge of the root disease centers. Both initial proportion of infected trees and the random start are included in significant interaction terms.

The sums of squares from table 3 are plotted as before against the cumulative chi-square distribution (fig. 4). The effect of P is still present as it was in the first cycle. The parameter I is not a large effect. The effects of N, A, and their interaction, NA, are now more dominant effects with

respect to tree mortality. These parameters had little effect on mortality in the first cycle.

Data from four different stands were used to replicate the simulation experiment. The analysis of each stand separately presents some insight to the variance a user may encounter when simulating a particular stand. Table 4 presents the analysis of variance table for the first of the test stands, 2025. There is no error term for testing significance in this table. The single-degree-of-freedom sum of squares can still be plotted against the chi-square distribution (fig. 5). The largest effects are those associated with the parameters P and A. This agrees with the combined analysis for the four test stands (fig. 4).

If we examine the other three stands the pattern is not constant. The analyses of variance are given in tables 5, 6 and 7 for stands 4023, 4019, and 4040. The single-degree-of-freedom sum of squares are plotted in figures 6, 7, and 8. For stands 2025 and 4023, the parameter P has the largest effect on tree mortality. In stands 4019 and 4040 the parameter N has the largest effect. The distribution of trees by species, size and the total density of trees are based on stand inventory data and change from one stand to the next. In the Western Root Disease Model some parameters will have greater or lesser effect on tree mortality due to the interaction of these parameters with the stand inventory. One can still conclude that the simulated tree mortality during the second cycle would be most likely strongly influenced by the effects P, A, and N for future simulations.

For each of the 10 cycles, we computed an analysis of variance for tree mortality in the area infected. Table 8 shows the summary of the significance levels for such analyses for the first five cycles and the tenth cycle. The proportion of root system infected P is significant only in the first two cycles (short-term effect). Initial area infected, A, and number of centers, N, have strong long-term effects, but are low in relative effectiveness in the first cycle.

Size of Area Infected

This criterion is another Western Root Disease Model summary output. A summary of the significance levels from the analyses of variance are presented in table 9. The effect of replication R is significant in the second, third, and tenth cycles. The interaction of the random starting value and the number of centers is also significant.

The random placement of root disease centers in the model stand structure and the random placement of trees within the model stand affect the area infected at the end of the second and third 10-year periods of simulation. There is also a strong interaction effect of R with the number of root disease centers. This is significant across all cycles. The number of centers, initial area infected, and the random starting value almost completely define the area infected at the end of the first 10-year cycle. Plotting the sum of squares for the effects against the chi-square distribution as before shows the relative importance of these parameters for the second, third and fifth cycles (figs. 9, 10, and 11). It is clear that for our range of starting values, the initial area infected and number of centers dominate the size of the area infected.

Merchantable Cubic Foot Volume

In the analyses for this criterion, in the infected area, a covariant is included in our design. The covariant is the merchantable cubic foot volume for the stand in 1983. This is computed from the inventory data and reduces much of the stand-to-stand variation. During the first simulation cycle the stocking level within the root diseased area begins the same as the stocking level in the rest of the stand. If in the inventory we know which sample points occur within the diseased areas and which do not, different stocking levels can be started for the infected area. The stocking-level difference between infected and noninfected areas of the stand become larger as the simulation progresses.

A summary of the significance levels from the analyses of covariance are given in table 10. Nine different parameters are significant ($\alpha = 0.05$) in the first cycle. The dominant parameters are initial rate of tree infection and percent root system colonized (fig. 12). By the third cycle things have changed (fig. 13). Initial rate of trees infected is the major effect; number of centers replaces percent roots colonized in relative effectiveness. After 50 years (the fifth cycle) the initial area infected is the dominant effect; however, number of centers continues as the second largest factor in ranking (fig. 14).

After 100 years, the effect of number of centers exceeds the initial area infected as an influence for the merchantable cubic foot volume present on the infected area of the stand (fig. 15). Such long-term projections should be viewed with caution; they indicate only trends. Some of the Western Root Disease Model simulations represent the disease spreading until the centers begin to overlap and even spread beyond the boundary of the stand. The starting conditions within a root disease center are of little significance for such long-term projections.

Summary of *Armillaria* Analyses

The initial area infected and the number of centers have the greatest and most widespread effects. They affect most stand attributes except the tree mortality during the first cycle. The number of centers is second to initial infected area in both size and range of effects. As an interaction these two terms are also significant for long-term effects. The proportions, trees infected, and root system colonized strongly affect the tree mortality for the first two cycles. Proportion of trees infected also affects the merchantable cubic foot volume within the disease area. Replication has a short-term effect on infected area. Through an interaction with number of centers it has a longer-term effect on infected area. The root disease parameters affecting the merchantable volume are initial area infected and number of centers.

Analyses for *Phellinus*

For *Phellinus* the results are similar. The corresponding set of figures for the squared effects against the chi-square distribution reveal almost the same ordering of effects (figs. 16-25, and tables 11-13). *Phellinus* differs from *Armillaria* in tree mortality. For *Phellinus* only the initial rate of in-

fection among trees in the stand has a significant effect on the mortality rate. This effect is significant for only the first cycle. Area initially infected with *Phellinus* and the numbers of centers are the more dominant effects on total infected area. This was true for *Armillaria* also. The pattern of significant factors is similar for *Phellinus* and *Armillaria*.

For long-term simulations with each root disease, the initial number of centers and the initial area infected determine the stand conditions. The *Phellinus* model will infect and kill some tree species at different rates from the *Armillaria* model. But given enough time the results are the same for the projected stand.

CARRYOVER MODEL

Model Overview

The Carryover Model is a submodel within the Western Root Disease Model. It is intended to bridge the short time period between the harvest of a stand and the regeneration of the next stand. During this time the host trees are chiefly seedlings to saplings. To understand why a submodel is needed, a quick review of the basic model is given.

In the basic Western Root Disease Model the host tree and nonhost tree density is provided by the stand inventory data. The user through KEYWORDS specifies the root disease conditions within the stand. The base model represents the stand as a square area, and the disease areas as circles within this square (figs. 1 and 2). Trees are generally distributed at random from the tree list to a second smaller characterization, which is a subset of the stand represented. Some trees within the disease area are designated at random as infected to match the user-specified parameters. The basic model then simulates the spread of the disease from one tree location to the adjacent ones. There are user options to control the root disease conditions more closely and the method of spread (Stage et al. 1990).

The basic model assumes there are sufficient trees and that their root systems would overlap enough for the disease to spread from one tree to its neighbors. This will not be the case during the stand regeneration period. Most of the host material will be seedlings whose root systems are too small to facilitate the spread of root disease. When the seedlings and saplings become small trees with root closure (overlap), the simulation can again be done under the base model.

Let us assume the harvest of a stand is simulated (clearcut). The inoculum is in infected tree stumps and is modeled to decay with time. Seedlings are simulated at random (natural regeneration) or systematic (planted) or both in the model's representation of the stand area. During this time period the spread of the disease is minimal. Placement of seedlings within influence of the decaying stumps is the prime mode for the continuance of the disease. The disease (density of infected trees) may decrease during this period. If the cycle length were left at 10 years, small trees could become infected, die, and decay before the end of the cycle. It is assumed this process will continue for 20 years. To allow for an "Establishment

Model" to run efficiently, this period is divided into four cycles of five years each (Ferguson and Crookston 1984). At the end of this period the stand will be modeled by the base model. This 20-year period is modeled by the Carryover submodel.

There are two restrictions on the Carryover Model. The first restriction concerns the basic model. If the tree density is still great enough for the basic model to spread the disease from tree-to-tree, the Carryover Model should not be used. This often happens after a thinning. The user may, however, still need to specify that the Carryover Model be used. An understory removal may create conditions where regeneration occurs. When this happens the seedlings are not seen by the Western Root Disease Model unless the Carryover Model is used.

The second restriction concerns the time period for the Carryover Model to operate. Usually this is 20 years or four 5-year cycles. The number of cycles is set by the user as a field on the CARRY keyword. The length of each cycle is set by the Prognosis keyword TIMEINT. These keywords must be set correctly. The field in the CARRY keyword specifies the number of cycles after stand entry for which the carryover model is to operate. If there is a second stand entry before this time has elapsed, the carryover period is continued for the specified number of cycles after this second entry. For example, a seed tree cut could require that the leave trees be removed 10 years after the first harvest. In our context this would be two 5-year cycles after the start of the Carryover Model. The Carryover Model would be extended until four cycles after the leave-trees are cut if the field on the CARRY keyword were left at the default of four. If it is set to two then the end of the carryover period is set to two cycles after the leave-trees are cut. Since this is also 4 cycles, or 20 years after the primary stand harvest, the model should work.

The scenario for evaluating the carryover process is limited to focus attention on the Western Root Disease Model parameters. A more complete evaluation would involve many Prognosis and Establishment Model attributes.

The same four stands that were used to test the base set of parameters are used to test the carryover process. Each stand is simulated as a stand inventoried in 1983, harvested in 1993, and examined in 2013 and every 10 years after for disease conditions. Each stand is assumed to be 23 acres in size and have a single 4-acre root disease center. Each will be clearcut in 1993 and burned in 1995. The four simulation cycles after harvest are of five years in length. The next 5 simulation cycles are 10 years in length, as is the first simulation cycle before harvest. Stand age is reset to 5 in 1998. Two inventories of the regeneration following harvest are made, TALLYONE in 1997 and TALLYTWO in 2007. These supply the new trees to both the Prognosis Model and the Western Root Disease Model.

The Establishment Model keyword PLANT will be used in the sensitivity analyses, along with the root disease model keywords RRINIT, RSEED, PSTUMP, and RRJUMP. Additional keywords are needed for these simulations but these represent constant conditions across all simulations (table 14).

Design and Analyses for *Armillaria*

For testing the Carryover Model a set of five parameters will be considered for *Armillaria*:

L, planting of a resistant species, western larch (*Larix occidentalis* Nutt.)

I, initial proportion of trees infected;

R, replication (random starts);

S, removal of stumps after harvest; and

J, jump in infected area following harvest.

For *Phellinus* only the first four of these parameters will be considered.

If we proceed as before then we have each of the 5 parameters taking on one of two values, forming a total of 32 treatment combinations. As in the previous exercise we have four stands as replications of the experiment. After computing the 128 simulations we proceed with the analyses of variance as our first-level test.

On the RRINIT keyword, all parameters but fields 3 and 4 are held constant. These fields (the number of infected trees and the number of uninfected trees per acre within the center) are used to set the initial infection rate among trees. This will represent a low of 5 percent infection and a high of 25 percent infected trees.

RSEED is again the random starting value for the root disease model and will be set to one of two values: 3941 or 28413.

PSTUMP has three fields. The first and third are held constant. The year that stumps are removed (field one) is 1994. The minimum diameter of stumps removed (field three) is 5 inches. The efficiency at which stump pushing is done (field two) is set to .01 for a low value and .95 for a high value. The low value simulates no deliberate effort to remove stumps after harvest. The higher value represents an attempt to remove all stumps of trees over 5 inches in diameter.

RRJUMP is a keyword to simulate the rapid spread of *Armillaria* in a newly cut stand. It has one field that is the number of tree radii for expansion of the root disease center following harvest. Because of our stipulation of the disease as one large center, the effect of this parameter is restricted. The low value in the test is one radii, the high value two radii.

The Establishment Model keyword PLANT is included in the sensitivity analysis. The simulation of root disease is dependent on the distribution of the host species. In this case the simulation of planting a resistant species can alter the expected spread of *Armillaria* and stocking of the stand. The PLANT keyword has four fields. The first, second, and fourth are held constant. The first is the date for planting, 1996. The second is the code for the species to be planted. Western larch is selected for planting in these tests. The fourth is the percent survival of the planted stock (80%). The third, the number of trees per acre planted, is set to zero, or 500 trees per acre.

Natural regeneration was simulated for each stand following harvest. Western larch comprised 27-39% of the stocking by year 2007 in our four test stands. The planting of 500 western larch raised the total stocking by an average of 469 trees per acre. Western larch became 40-48% of the stocking in 2007.

Trees Per Acre Infected

The first criterion examined is the number of infected trees per acre within the infected area. This criterion is evaluated for the new stand at age 30, 40, 50, 60, and 70. At age 30 there have been 5 simulation cycles since harvest and the Carryover Model is no longer in effect. The summary of the significance levels from the analyses of variance is presented in table 15.

The only parameter significant ($\alpha = 0.05$) in table 15 is the removal of stumps, S. For the stand age of 30, only the two interactions LI (planting of resistant species by initial proportion of trees infected) and LIS (planting of resistant species by initial proportion of trees infected by removal of stumps after harvest) approach this significance level. Their relative effects are better seen in figure 26, where the one-degree-of-freedom sums of squares are plotted against the chi-square distribution.

The carryover of root disease to a new stand following harvest depends on the distribution of infection among trees in the old stand and the size distribution of these infected trees. In this respect, the variation among our four test stands is great. In stand 4019 with light infection (5 percent of the trees in the disease center), the removal of stumps (95 percent) was sufficient to prevent the establishment of *Armillaria* in the new stand in some simulations. In stand 2025, *Armillaria* failed to carry over in the new stand for all combinations of light infection and stump removal. In stand 4023 the simulation of stump removal was sufficient at removing the disease even for high levels of initial infection. *Armillaria* failed to carry over in any of the simulations for stand 4040. This stand was the youngest at harvest and had the fewest large diameter trees.

Area Infected

This criterion is significantly affected by the percent of the trees infected in the old stand and the removal of stumps. These two parameters are significant across all stand ages examined (table 16). Figure 27 shows the one-degree-of-freedom sum of squares plotted against the chi-square distribution for stand age 30.

Number of Infection Centers

The number of root disease centers simulated for the new stand is held constant in the model once it is calculated by the Carryover Model. In this test the Carryover Model evaluates the new stand condition at four cycles after cutting. For this criterion, the number of infection centers in the new stand is affected by the removal of stumps and the percent of trees infected in the old stand (table 17, fig. 28).

Design and Analyses for *Phellinus*

The Carryover Model for *Phellinus* is very different than for *Armillaria*. First, *Phellinus* is assumed not to further colonize the root system of its host tree if this tree is cut. The keyword RRJUMP therefore has no effect when *Phellinus*

is simulated. Second, the life span of the inoculum for a stump is a minimum of 20 years for *Phellinus*. After this the inoculum quickly decreases as the stump decays. So while the model simulates a decrease in inoculum for the carryover period for *Armillaria*, there is no decrease for *Phellinus*. One can still remove stumps, PSTUMP. But it is unlikely to remove small stumps in this way. Trees less than 5 inches dbh can supply sufficient inoculum for infection of the new stand. Western larch is not as resistant to *Phellinus* as it is to *Armillaria*.

The user-specified parameters to be tested for *Phellinus* and the Carryover Model are:

- L, planting of a relatively resistant species, western larch;
- I, initial proportion of trees infected;
- R, replication (random starts); and
- S, removal of stumps.

As in previous experiments, the starting parameter for RSEED will be either 3941 or 28413.

The initial proportion of trees infected within the root disease area of the stand will be controlled by the third field in the keyword RRINIT. The low rate is 5 percent infection and the high rate is 25 percent infection.

The stump pushing will remove either a low proportion of 0.01 or a high of 0.95. Only stumps from trees with a diameter of 5 inches or more are removed by stump pushing.

Planting is represented by a single parameter. The high level is to plant 500 western larch per acre and the low level is to plant none.

This gives our experiment four parameters, each with two levels. There are also four stands for replication. The simulations follow the pattern set for the *Armillaria* experiment. The stands are inventoried in 1983, harvested in 1993, burned in 1995, and planted in 1996. Each stand is modeled as being 23 acres in size with a single 4-acre root disease center in 1983. The simulations will be evaluated after the Carryover Model is over and the new stand is age 30, 40, 50, 60, and 70 years of age.

Trees Per Acre Infected

For this first criterion, analysis of variance is used as before with all factors considered fixed except stands. The significance levels from testing each year separately are given in table 18. The sum of squares are plotted against the chi-square distribution for the analysis of the response at stand age 30 (fig. 29). The only parameters of statistical significance at stand age 30 are the planting of western larch and initial percent of trees infected. By stand age 40 the points do not depart greatly from the straight line pattern suggested by the chi-square distribution (fig. 30). This of course agrees with our analysis of variance tests.

Area Infected

Area infected in the new stand is the next criterion examined. Due to the model keeping the *Phellinus* inoculum available for 20 years as a minimum, there are many small sources for infection at the end of the carryover period. Many small, new centers are simulated to replace

the one large center from the previous stand. Variation in total area infected at age 30 for the new stand is small. Due to the large perimeter for such a small total area, the centers are simulated to spread quickly until they begin to overlap. A summary of the significance levels from the analysis of variance is given in table 19. The planting of western larch is the most effective parameter. The single-degree-of-freedom sum of squares is plotted in figure 31. This plot allows us to do no more than identify the planting of larch as a significant parameter. Initial infection rate plus removal of stumps have a significant but much smaller effect (fig. 31). The significance of these parameters is better determined from the analysis of variance. Plotting the single-degree-of-freedom sum of squares helps us see the relative effect when several parameters are significant and allows us to make an assessment without an error term for our model. But plotting cannot create effects where there are none.

Number of Infection Centers

The number of root disease centers in the new stand as recorded in year 2023 is the last criterion considered. The parameters for planting western larch and initial infection rate plus the interaction of these two parameters are significant (table 20, fig. 32).

Summary of Planting Western Larch

The planting of western larch had a significant effect on the simulation of stands with *Armillaria* or *Phellinus*. The change in the simulations is very different for the two diseases. Western larch has a low probability of infection (0.05) by *Armillaria* in the model as compared to 0.50 for Douglas-fir (*Pseudotsuga menziesii*) or 0.60 for grand fir

(*Abies grandis*). The simulation of planting 500 western larch per acre in a stand infected with *Armillaria* results in a significant decrease in the area infected despite the fact that the new stand is more densely stocked.

Western larch has a moderate probability of infection (0.20) with *Phellinus* in the model compared to Douglas-fir (0.40) or grand fir (0.40). The simulation of planting 500 western larch in stands infected with *Phellinus* results in a significant increase in the area infected and the number of centers in the new stand.

GENERAL CONCLUSIONS

In general, the models for both *Armillaria* and *Phellinus* are sensitive to the same user-specified parameters. For short-term simulations of 10-20 years, several stand conditions are sensitive to the initial proportion of trees infected and the proportion of root systems colonized. For long-term simulations, 30-50 years, the stand conditions are sensitive to the initial area infected and the number of centers.

For the Carryover Model, the planting of a resistant species and the removal of stumps are the strong effects. In the model, *Phellinus* will be carried over to infect the new stand after a harvest. *Armillaria* will be carried over to the new stand if large infected stumps are left after harvest. It is always necessary to simulate the right root disease for a stand; during carryover, the diseases behave very differently.

The Western Root Disease Model will be revised as new information on *Armillaria* and *Phellinus* becomes available. Sensitivity analysis like this one should be a part of future model testing.

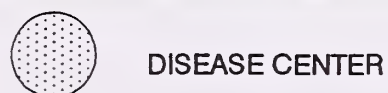
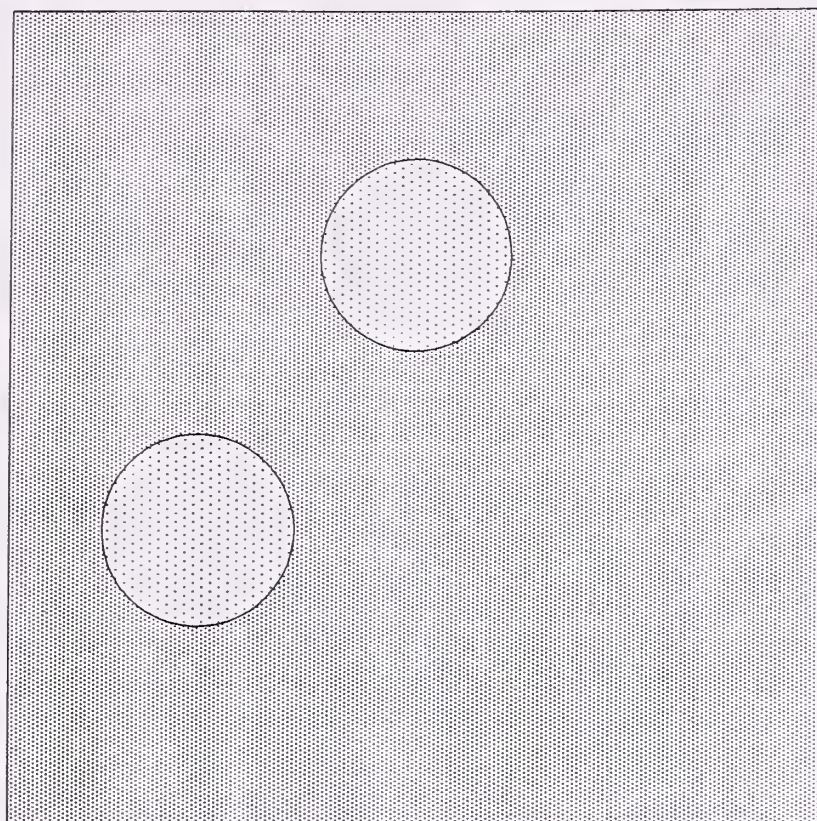


Figure 1.—Two acres and 2 root disease centers in a 23-acre stand as simulated by the Western Root Disease Model.

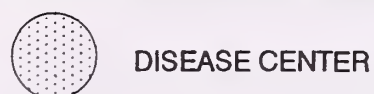
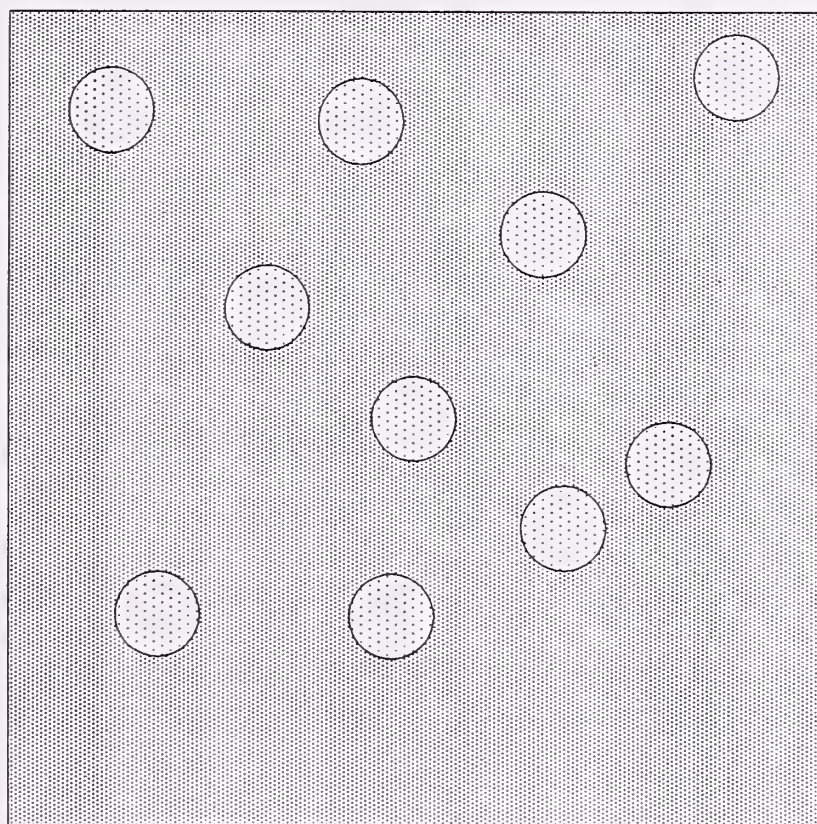


Figure 2.—Two acres and 10 root disease centers in a 23-acre stand as simulated by the Western Root Disease Model.

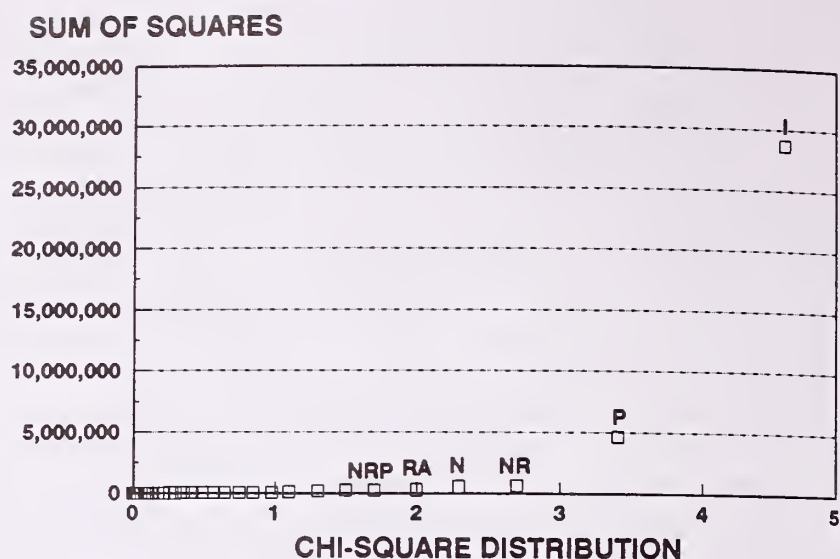


Figure 3.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Armillaria* in first cycle.

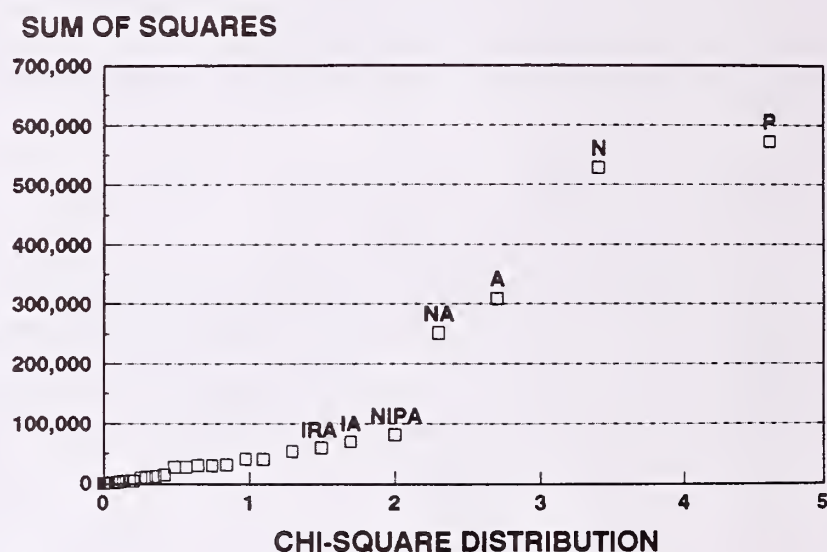


Figure 4.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Armillaria* in second cycle.

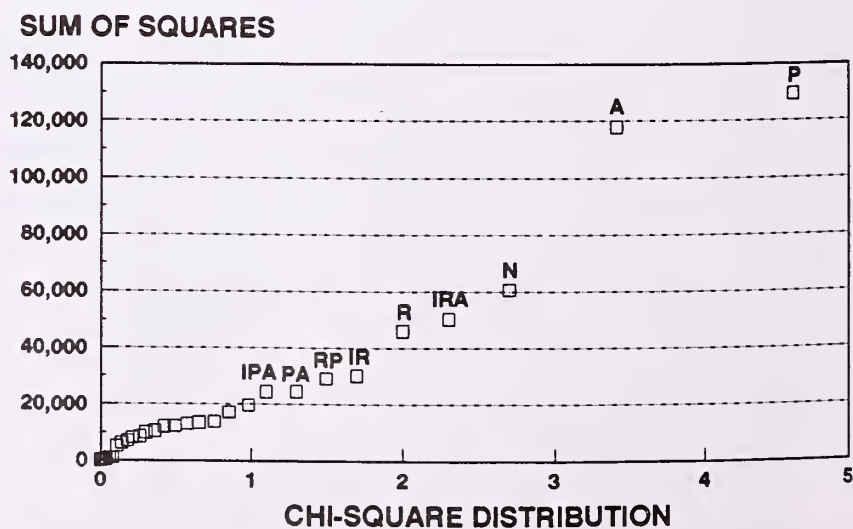


Figure 5.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Armillaria* in second cycle for stand 2025.

SUM OF SQUARES

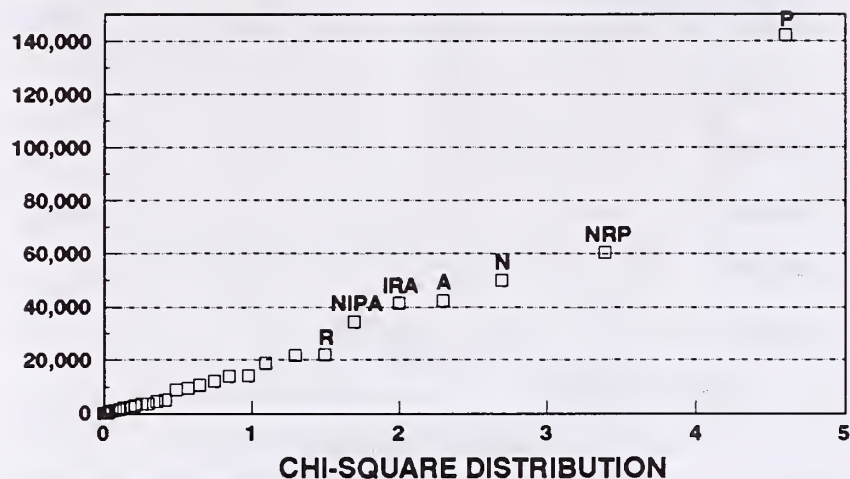


Figure 6.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Armillaria* in second cycle for stand 4023.

SUM OF SQUARES

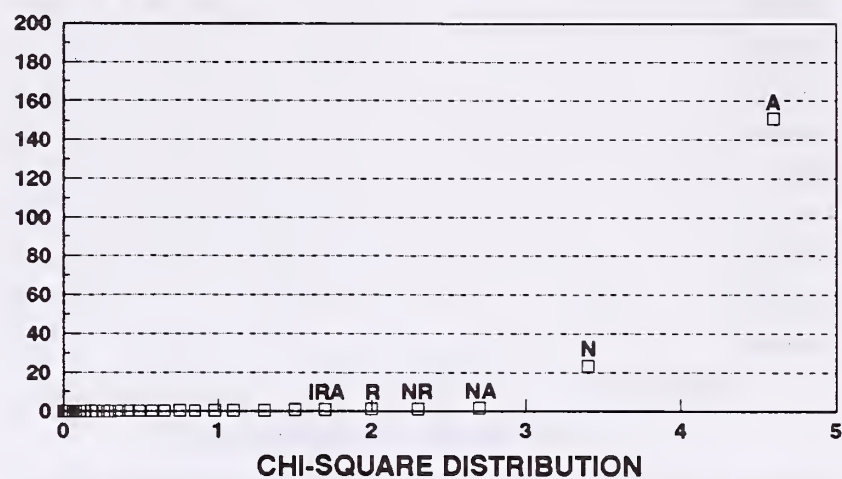


Figure 9.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Armillaria* in second cycle.

SUM OF SQUARES

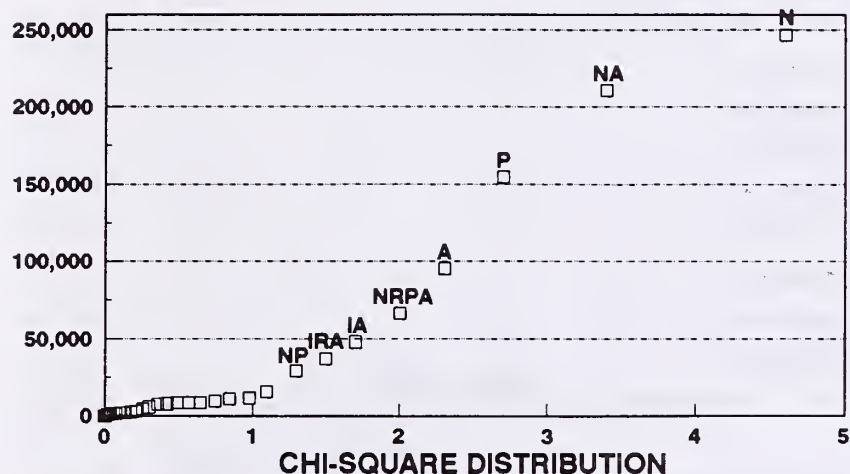


Figure 7.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Armillaria* in second cycle for stand 4019.

SUM OF SQUARES

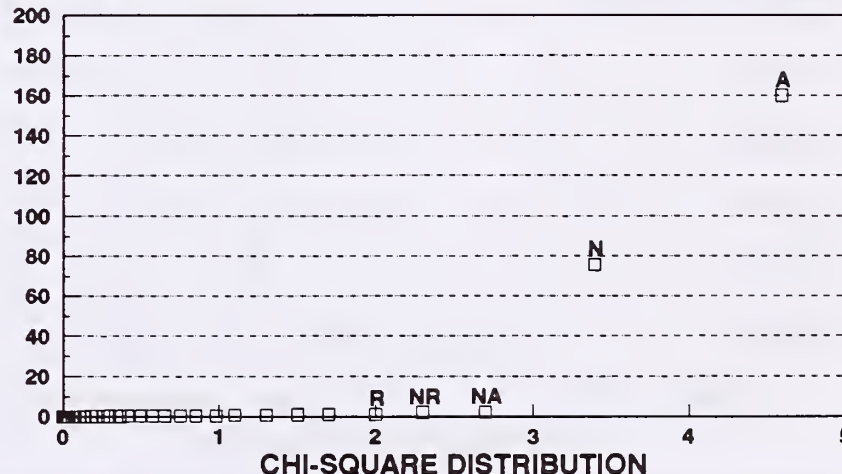


Figure 10.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Armillaria* in third cycle.

SUM OF SQUARES

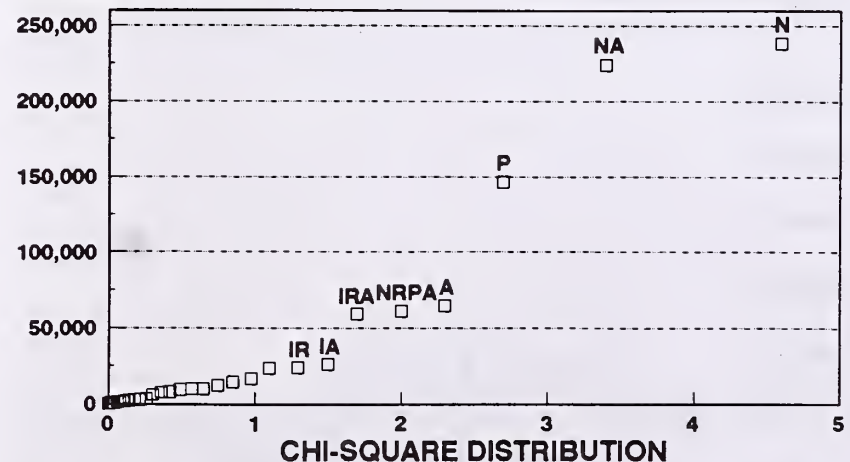


Figure 8.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Armillaria* in second cycle for stand 4040.

SUM OF SQUARES

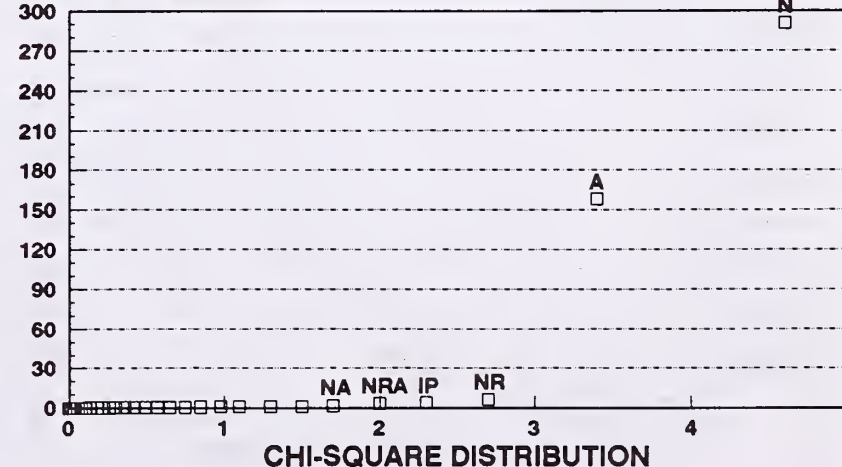


Figure 11.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Armillaria* in fifth cycle.

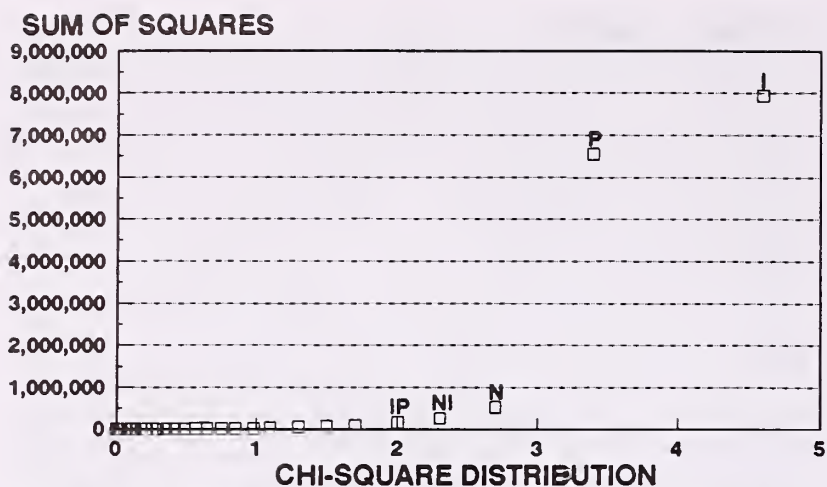


Figure 12.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Armillaria*-infected area in first cycle.

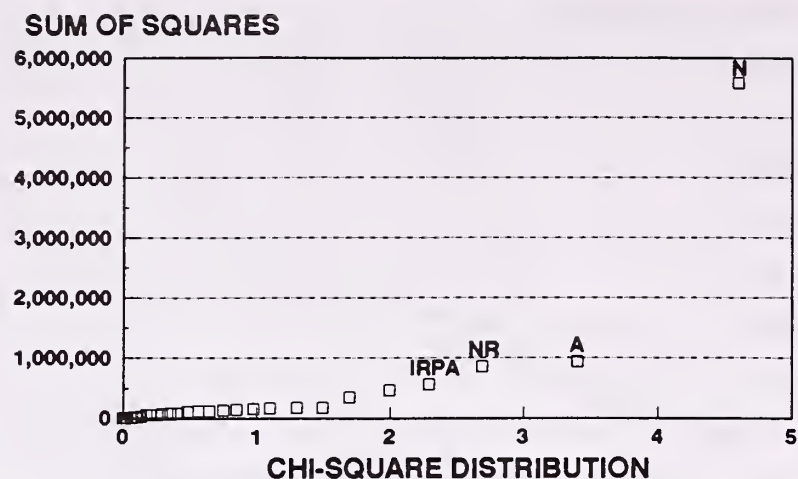


Figure 15.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Armillaria*-infected area in tenth cycle.

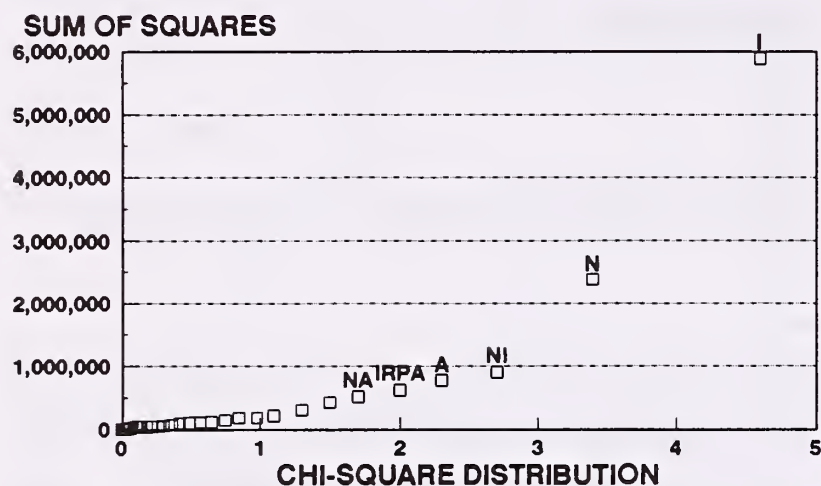


Figure 13.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Armillaria*-infected area in third cycle.

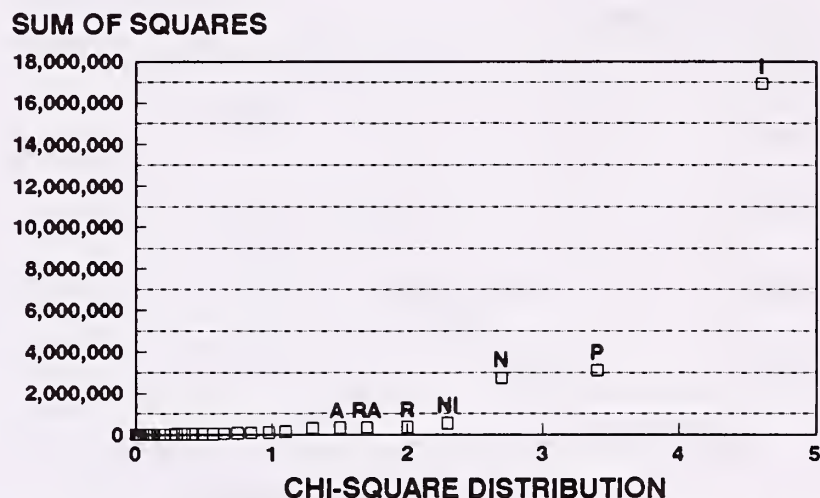


Figure 16.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Phellinus* in first cycle.

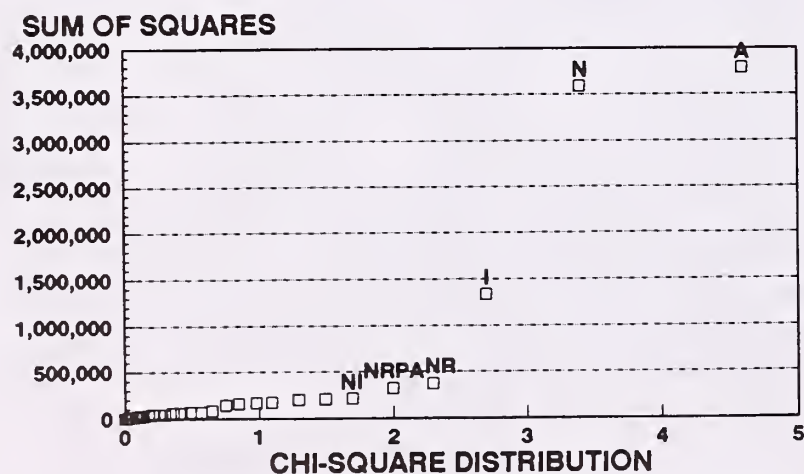


Figure 14.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Armillaria*-infected area in fifth cycle.

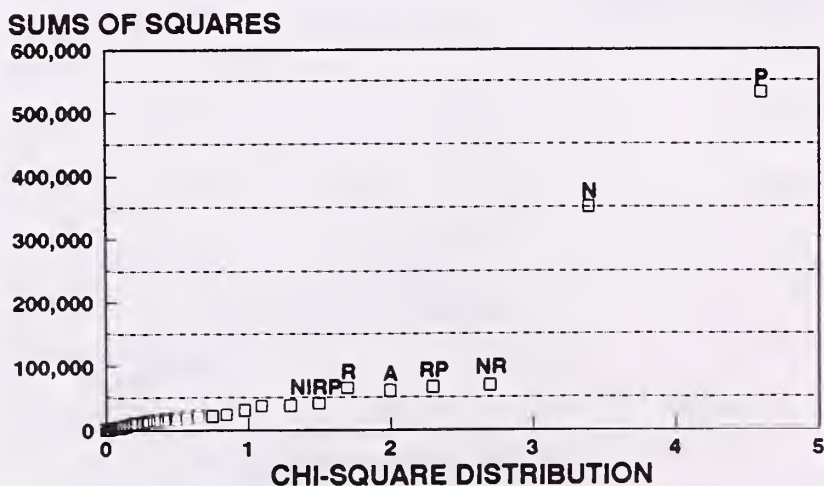


Figure 17.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Phellinus* in second cycle.

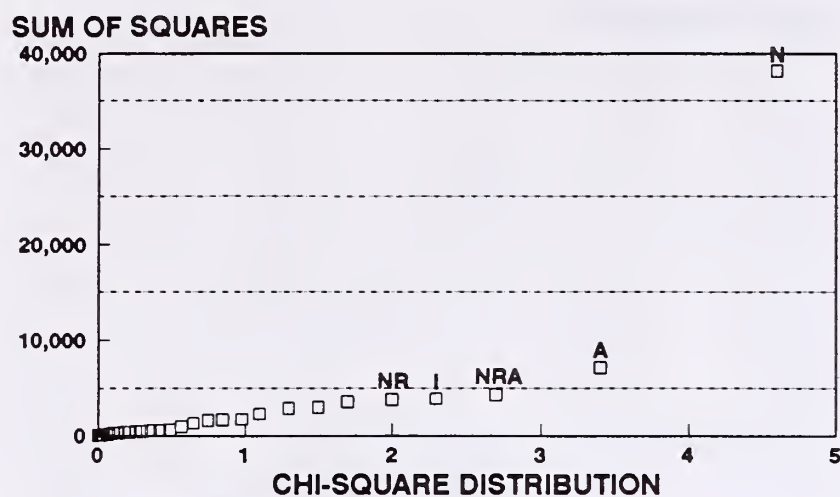


Figure 18.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for tree mortality due to *Phellinus* in fifth cycle.

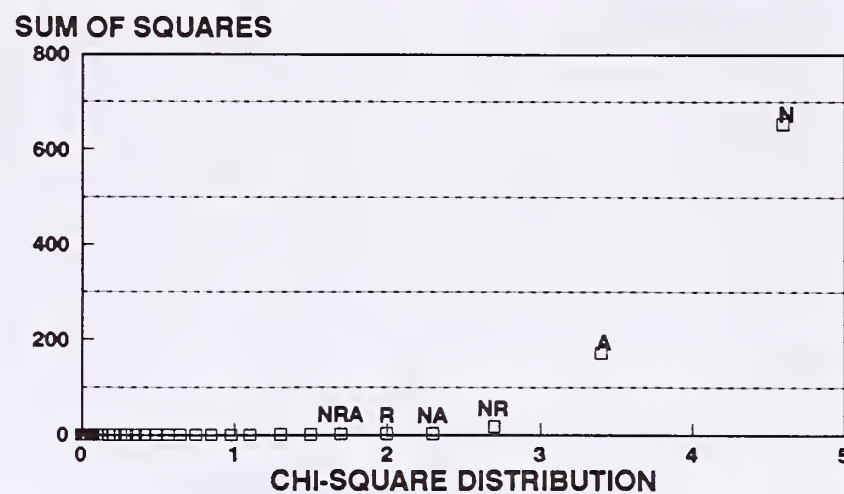


Figure 21.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Phellinus* in fifth cycle.

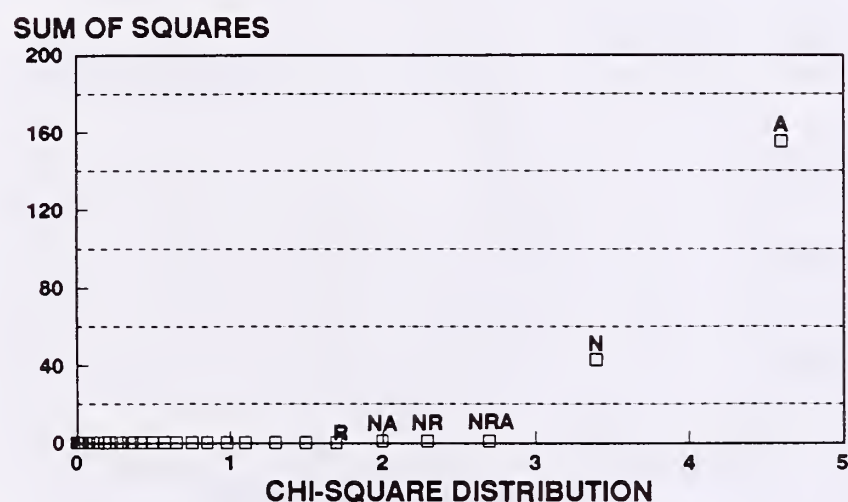


Figure 19.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Phellinus* in first cycle.

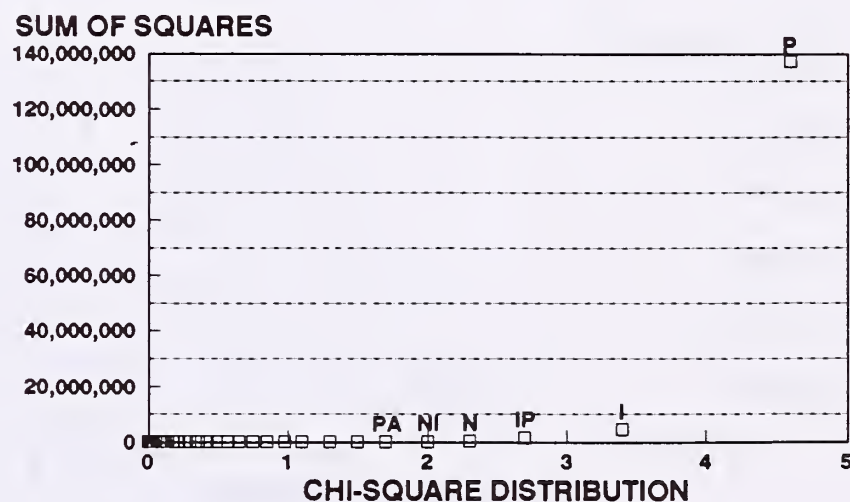


Figure 22.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Phellinus*-infected area in first cycle.

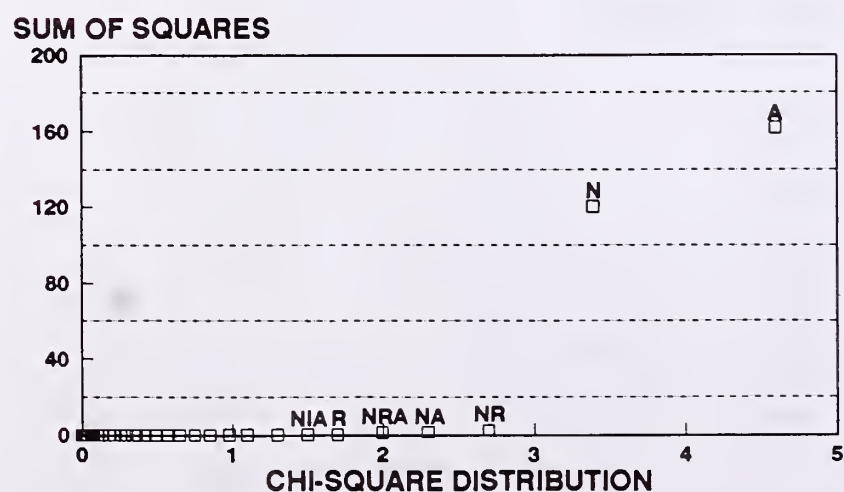


Figure 20.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Phellinus* in second cycle.

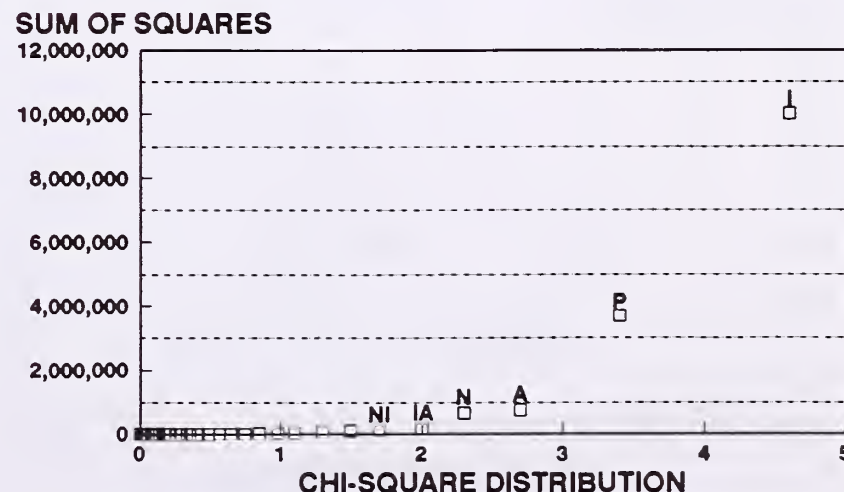


Figure 23.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Phellinus*-infected area in second cycle.

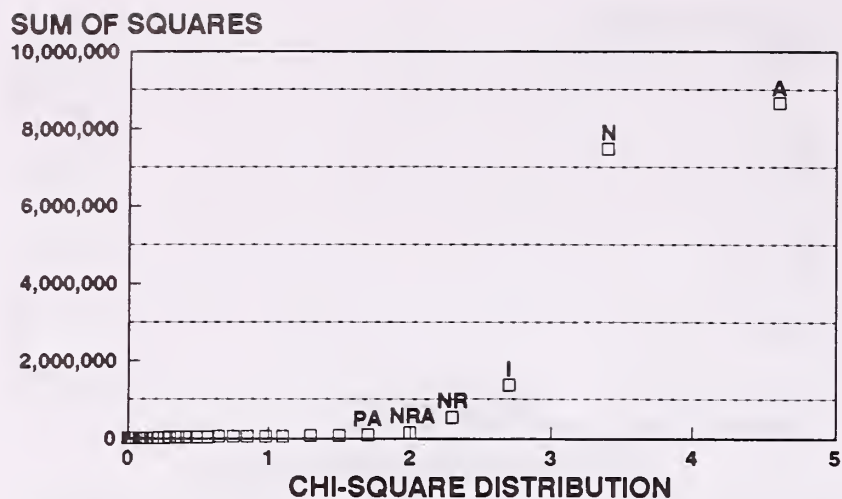


Figure 24.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Phellinus* infected area in fifth cycle.

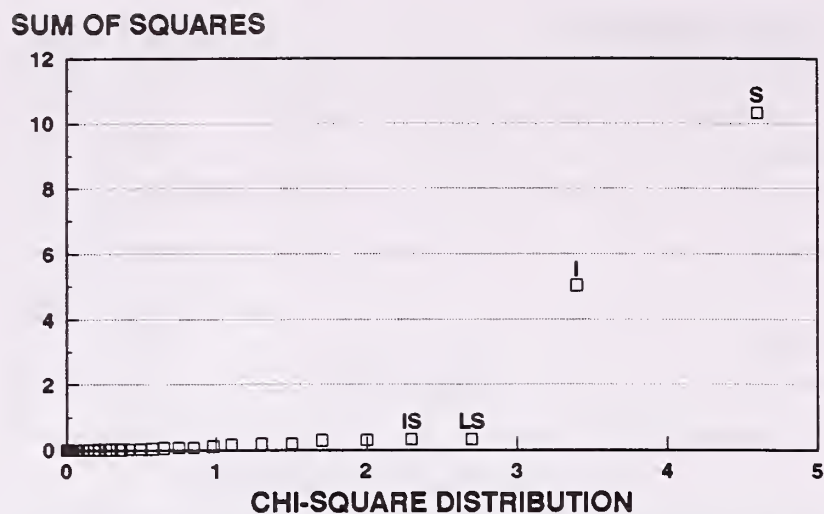


Figure 27.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Armillaria* at stand age 30.

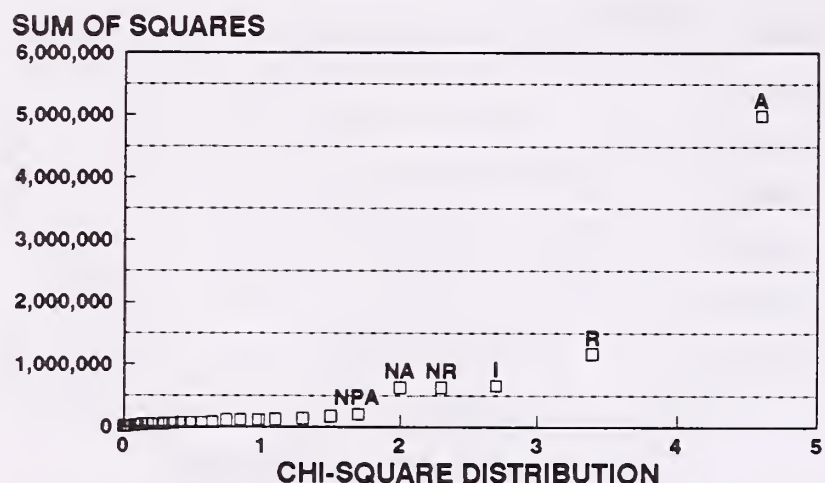


Figure 25.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for merchantable volume in *Phellinus*-infected area in tenth cycle.

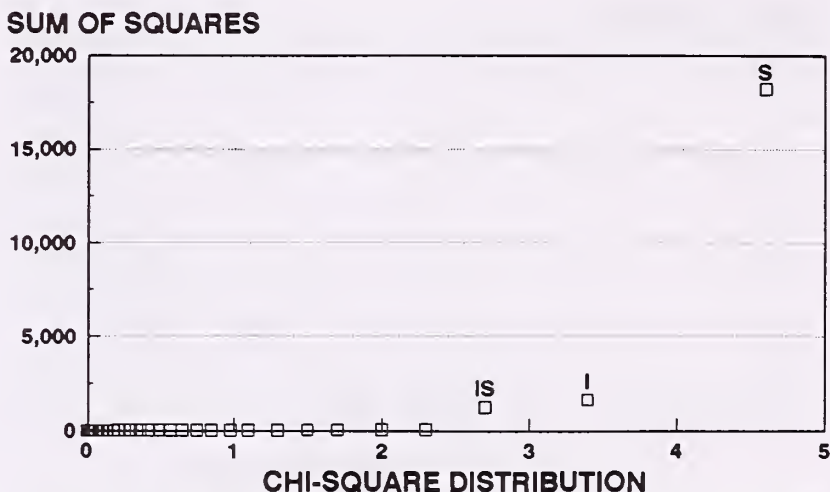


Figure 28.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for number of *Armillaria* centers at stand age 30.

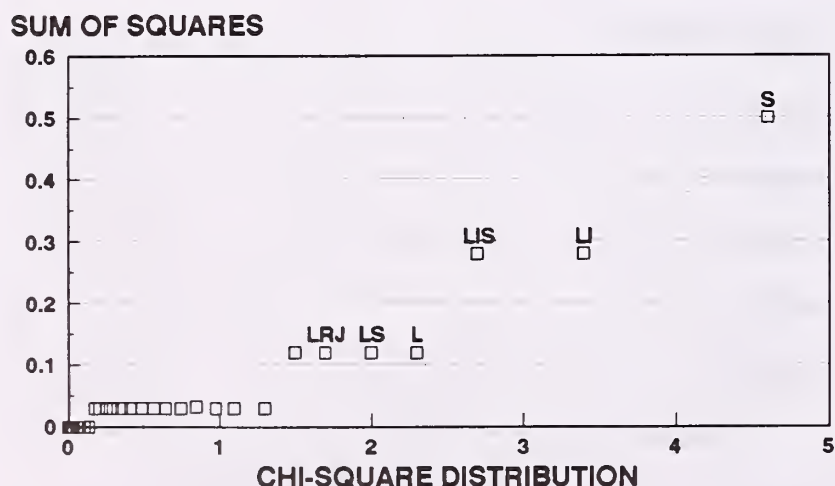


Figure 26.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected trees per acre in *Armillaria* centers at stand age 30.

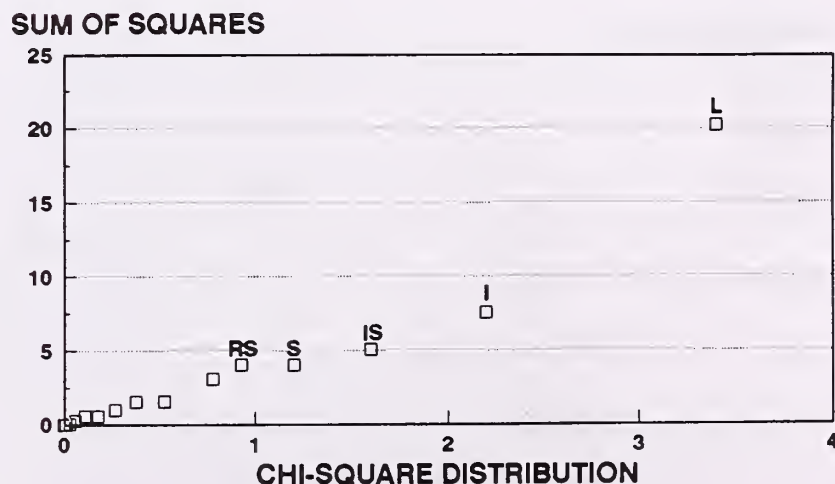


Figure 29.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected trees per acre in *Phellinus* centers at stand age 30.

SUM OF SQUARES

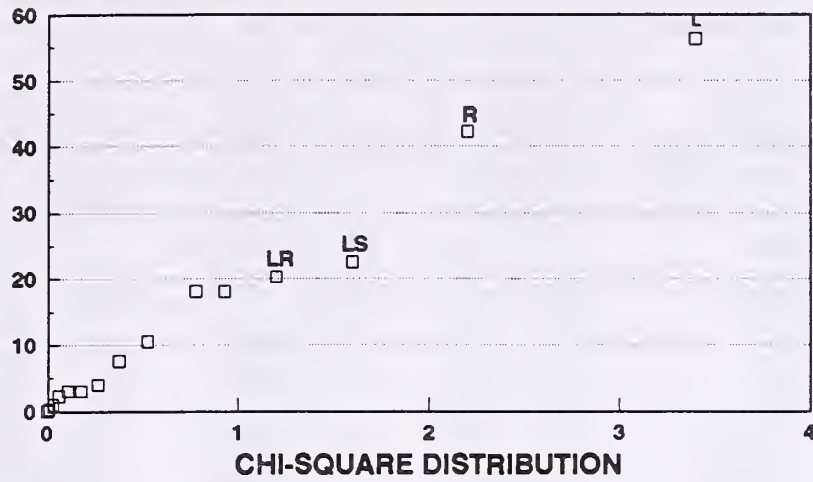


Figure 30.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected trees per acre in *Phellinus* centers at stand age 40.

SUM OF SQUARES

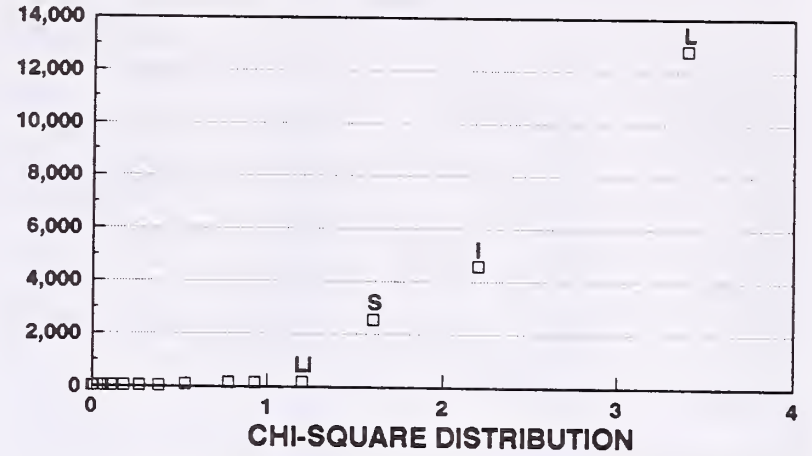


Figure 32.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for number of *Phellinus* centers at stand age 30.

SUM OF SQUARES

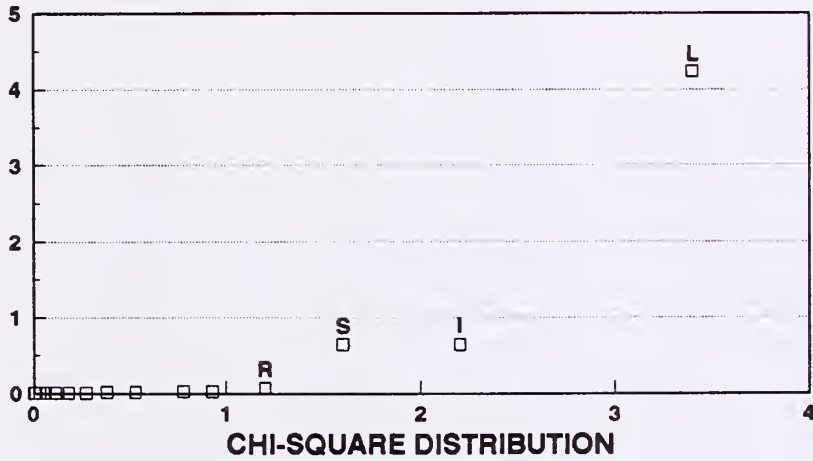


Figure 31.—Single-degree-of-freedom sum of squares plotted against the chi-square distribution for infected area due to *Phellinus* at stand age 30.

Table 1.—Keywords for Prognosis and Basic Western Root Disease Models.

| | | | | | | | | | |
|---|-------|-----|-------|----|-----|----|---|---|--|
| NUMCYCLE | 10 | | | | | | | | |
| INVYEAR | 1983 | | | | | | | | |
| COMMENT | | | | | | | | | |
| SCALE | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | |
| END | | | | | | | | | |
| RRIN | | | | | | | | | |
| RRTYPE | 1 | | | | | | | | |
| SPREAD | 1 | | | | | | | | |
| RRINIT | 0 | 2 | 1 | 19 | .20 | 2 | | | |
| SAREA | 23 | | | | | | | | |
| RSEED | 3941. | | | | | | | | |
| RRECHO | | | | | | | | | |
| END | | | | | | | | | |
| ECHOSUM | | | | | | | | | |
| STDIDENT | | | | | | | | | |
| CROW CREEK STAND 2025 | | | | | | | | | |
| DESIGN | 40 | 300 | 5.000 | 7 | 0 | 1 | | | |
| STDINFO | 116 | 530 | 130 | 45 | 10 | 33 | | | |
| GROWTH | 0 | 5 | | | | | | | |
| TREEFMT | | | | | | | | | |
| (13X,I4,T18,I4,T28,F2.0,T30,I1,T33,A2,F3.1,F2.1,3X,F3.0,T43,F3.0,T54,F2.0,T46,I1,T48,3(I2,I1),T22,I1,T22,I1,T63,I2,I3,I3,I1,I1) | | | | | | | | | |
| PROCESS | | | | | | | | | |
| STOP | | | | | | | | | |

Table 3.—Analysis of variance for tree mortality rate in second cycle, 2003, for *Armillaria*-infected stands.

| Source of Variation | SS | DF | MS | F | Sig of F |
|-----------------------|-------------|----|-------------|---------|----------|
| Within Cells | 1381286.75 | 96 | 14388.40 | | |
| Constant | 16485999.76 | 1 | 16485999.76 | 1145.78 | .000 |
| N N-centers | 528520.51 | 1 | 528520.51 | 36.73 | .000 |
| I I-% trees infected | 9265.01 | 1 | 9265.01 | .64 | .424 |
| R R-random start | 31343.82 | 1 | 31343.82 | 2.18 | .143 |
| P P-% roots infected | 572048.82 | 1 | 572048.82 | 39.76 | .000 |
| A A-area infected | 309389.45 | 1 | 309389.45 | 21.50 | .000 |
| N BY I | 2511.63 | 1 | 2511.63 | .17 | .677 |
| N BY R | 4016.32 | 1 | 4016.32 | .28 | .598 |
| N BY P | 9677.88 | 1 | 9677.88 | .67 | .414 |
| N BY A | 251251.88 | 1 | 251251.88 | 17.46 | .000 |
| I BY R | 13.13 | 1 | 13.13 | .00 | .976 |
| I BY P | 3993.95 | 1 | 3993.95 | .28 | .600 |
| I BY A | 69611.13 | 1 | 69611.13 | 4.84 | .030 |
| R BY P | 29859.57 | 1 | 29859.57 | 2.08 | .153 |
| R BY A | 10.70 | 1 | 10.70 | .00 | .978 |
| P BY A | 13715.82 | 1 | 13715.82 | .95 | .331 |
| N BY I BY R | 182.88 | 1 | 182.88 | .01 | .910 |
| N BY I BY P | 114.38 | 1 | 114.38 | .01 | .929 |
| N BY I BY A | 26536.32 | 1 | 26536.32 | 1.84 | .178 |
| N BY R BY P | 52853.13 | 1 | 52853.13 | 3.67 | .058 |
| N BY R BY A | 1397.88 | 1 | 1397.88 | .10 | .756 |
| N BY P BY A | 11007.57 | 1 | 11007.57 | .77 | .384 |
| I BY R BY P | 27173.63 | 1 | 27173.63 | 1.89 | .173 |
| I BY R BY A | 59641.95 | 1 | 59641.95 | 4.15 | .045 |
| I BY P BY A | 244.76 | 1 | 244.76 | .02 | .897 |
| R BY P BY A | 40292.51 | 1 | 40292.51 | 2.80 | .097 |
| N BY I BY R BY P | 40505.70 | 1 | 40505.70 | 2.82 | .097 |
| N BY I BY R BY A | 1158.01 | 1 | 1158.01 | .08 | .777 |
| N BY I BY P BY A | 82367.26 | 1 | 82367.26 | 5.72 | .019 |
| N BY R BY P BY A | 29737.51 | 1 | 29737.51 | 2.07 | .154 |
| I BY R BY P BY A | 3454.88 | 1 | 3454.88 | .24 | .625 |
| N BY I BY R BY P BY A | 388.51 | 1 | 388.51 | .03 | .870 |

Table 2.—Analysis of variance for tree mortality rate in the first cycle, 1993, for *Armillaria*-infected stands.

| Source of variation | SS | DF | MS | F | Sig of F |
|-----------------------|--------------|----|--------------|---------|----------|
| Within cells | 15473799.75 | 96 | 161185.41 | | |
| Constant | 271762555.30 | 1 | 271762555.30 | 1686.02 | .000 |
| N - centers | 527749.70 | 1 | 527749.70 | 3.27 | .074 |
| I - % trees infected | 28695047.07 | 1 | 28695047.07 | 178.03 | .000 |
| R - random start | 59125.01 | 1 | 59125.01 | .37 | .546 |
| P - % roots infected | 4631065.70 | 1 | 4631065.70 | 28.73 | .000 |
| A - area infected | 165672.07 | 1 | 165672.07 | 1.03 | .313 |
| N BY I | 217552.57 | 1 | 217552.57 | 1.35 | .248 |
| N BY R | 617021.63 | 1 | 617021.63 | 3.83 | .053 |
| N BY P | 65295.95 | 1 | 65295.95 | .41 | .526 |
| N BY A | 61732.20 | 1 | 61732.20 | .38 | .537 |
| I BY R | 40648.13 | 1 | 40648.13 | .25 | .617 |
| I BY P | 55569.45 | 1 | 55569.45 | .34 | .558 |
| I BY A | 897.82 | 1 | 897.82 | .01 | .941 |
| R BY P | 6713.51 | 1 | 6713.51 | .04 | .839 |
| R BY A | 272968.13 | 1 | 272968.13 | 1.69 | .196 |
| P BY A | 3665.82 | 1 | 3665.82 | .02 | .880 |
| N BY I BY R | 6859.13 | 1 | 6859.13 | .04 | .837 |
| N BY I BY P | 35.07 | 1 | 35.07 | .00 | .988 |
| N BY I BY A | 60421.57 | 1 | 60421.57 | .37 | .542 |
| N BY R BY P | 229926.76 | 1 | 229926.76 | 1.43 | .235 |
| N BY R BY A | 51.26 | 1 | 51.26 | .00 | .986 |
| N BY P BY A | 9852.57 | 1 | 9852.57 | .06 | .805 |
| I BY R BY P | 41.63 | 1 | 41.63 | .00 | .987 |
| I BY R BY A | 56490.01 | 1 | 56490.01 | .35 | .555 |
| I BY P BY A | 20075.07 | 1 | 20075.07 | .12 | .725 |
| R BY P BY A | 6742.51 | 1 | 6742.51 | .04 | .838 |
| N BY I BY R BY P | 12780.01 | 1 | 12780.01 | .08 | .779 |
| N BY I BY R BY A | 113228.51 | 1 | 113228.51 | .70 | .404 |
| N BY I BY P BY A | 20680.70 | 1 | 20680.70 | .13 | .721 |
| N BY R BY P BY A | 508.01 | 1 | 508.01 | .00 | .955 |
| I BY R BY P BY A | 41724.38 | 1 | 41724.38 | .26 | .612 |
| N BY I BY R BY P BY A | 6286.01 | 1 | 6286.01 | .04 | .844 |

Table 4.—Analysis of variance for tree mortality rate in second cycle, 2003, for *Armillaria* in stand 2025.

| Source of variation | SS | DF | MS | F | Sig of F |
|-----------------------|------------|----|------------|---|----------|
| Residual | .00 | 0 | | | |
| Constant | 3064669.03 | 1 | 3064669.03 | . | . |
| N - centers | 60639.03 | 1 | 60639.03 | . | . |
| I - % trees infected | 6244.03 | 1 | 6244.03 | . | . |
| R - random start | 45980.28 | 1 | 45980.28 | . | . |
| P - % roots infected | 129413.28 | 1 | 129413.28 | . | . |
| A - area infected | 117976.53 | 1 | 117976.53 | . | . |
| N BY I | 225.78 | 1 | 225.78 | . | . |
| N BY R | 8160.03 | 1 | 8160.03 | . | . |
| N BY P | 7050.78 | 1 | 7050.78 | . | . |
| N BY A | 1023.78 | 1 | 1023.78 | . | . |
| I BY R | 30073.78 | 1 | 30073.78 | . | . |
| I BY P | 205.03 | 1 | 205.03 | . | . |
| I BY A | 13407.03 | 1 | 13407.03 | . | . |
| R BY P | 29100.78 | 1 | 29100.78 | . | . |
| R BY A | 12051.28 | 1 | 12051.28 | . | . |
| P BY A | 24586.53 | 1 | 24586.53 | . | . |
| N BY I BY R | 1001.28 | 1 | 1001.28 | . | . |
| N BY I BY P | 270.28 | 1 | 270.28 | . | . |
| N BY I BY A | 13081.53 | 1 | 13081.53 | . | . |
| N BY R BY P | 19651.53 | 1 | 19651.53 | . | . |
| N BY R BY A | 5125.78 | 1 | 5125.78 | . | . |
| N BY P BY A | 11.28 | 1 | 11.28 | . | . |
| I BY R BY P | 9835.03 | 1 | 9835.03 | . | . |
| I BY R BY A | 50323.78 | 1 | 50323.78 | . | . |
| I BY P BY A | 24365.28 | 1 | 24365.28 | . | . |
| R BY P BY A | 13819.53 | 1 | 13819.53 | . | . |
| N BY I BY R BY P | 8482.53 | 1 | 8482.53 | . | . |
| N BY I BY R BY A | 457.53 | 1 | 457.53 | . | . |
| N BY I BY P BY A | 17066.28 | 1 | 17066.28 | . | . |
| N BY R BY P BY A | 12207.03 | 1 | 12207.03 | . | . |
| I BY R BY P BY A | 215.28 | 1 | 215.28 | . | . |
| N BY I BY R BY P BY A | 10404.03 | 1 | 10404.03 | . | . |

Table 5.—Analysis of variance for tree mortality rate in second cycle, 2003, for *Armillaria* in stand 4023.

| Source of variation | SS | DF | MS | F | Sig of F |
|-----------------------|------------|----|------------|---|----------|
| Residual | .00 | 0 | | | |
| Constant | 2794839.03 | 1 | 2794839.03 | | |
| N - centers | 49849.03 | 1 | 49849.03 | | |
| I - % trees infected | 11973.78 | 1 | 11973.78 | | |
| R - random start | 21997.53 | 1 | 21997.53 | | |
| P - % roots infected | 142177.78 | 1 | 142177.78 | | |
| A - area infected | 42413.28 | 1 | 42413.28 | | |
| N BY I | 4925.28 | 1 | 4925.28 | | |
| N BY R | 1262.53 | 1 | 1262.53 | | |
| N BY P | 87.78 | 1 | 87.78 | | |
| N BY A | 10548.78 | 1 | 10548.78 | | |
| I BY R | 75.03 | 1 | 75.03 | | |
| I BY P | 132.03 | 1 | 132.03 | | |
| I BY A | 1001.28 | 1 | 1001.28 | | |
| R BY P | 2869.03 | 1 | 2869.03 | | |
| R BY A | 18769.53 | 1 | 18769.53 | | |
| P BY A | 9282.03 | 1 | 9282.03 | | |
| N BY I BY R | 8745.03 | 1 | 8745.03 | | |
| N BY I BY P | 2064.03 | 1 | 2064.03 | | |
| N BY I BY A | 13902.78 | 1 | 13902.78 | | |
| N BY R BY P | 60465.03 | 1 | 60465.03 | | |
| N BY R BY A | 205.03 | 1 | 205.03 | | |
| N BY P BY A | 4441.53 | 1 | 4441.53 | | |
| I BY R BY P | 52.53 | 1 | 52.53 | | |
| I BY R BY A | 41256.28 | 1 | 41256.28 | | |
| I BY P BY A | 442.53 | 1 | 442.53 | | |
| R BY P BY A | 14070.03 | 1 | 14070.03 | | |
| N BY I BY R BY P | 21684.03 | 1 | 21684.03 | | |
| N BY I BY R BY A | 3465.28 | 1 | 3465.28 | | |
| N BY I BY P BY A | 34256.53 | 1 | 34256.53 | | |
| N BY R BY P BY A | 2432.53 | 1 | 2432.53 | | |
| I BY R BY P BY A | 3633.78 | 1 | 3633.78 | | |
| N BY I BY R BY P BY A | 1526.28 | 1 | 1526.28 | | |

Table 7.—Analysis of variance for tree mortality rate in second cycle, 2003, for *Armillaria* in stand 4040.

| Source of variation | SS | DF | MS | F | Sig of F |
|-----------------------|------------|----|------------|---|----------|
| Residual | .00 | 0 | | | |
| Constant | 5380020.03 | 1 | 5380020.03 | | |
| N - centers | 238222.53 | 1 | 238222.53 | | |
| I - % trees infected | 603.78 | 1 | 603.78 | | |
| R - random start | 148.78 | 1 | 148.78 | | |
| P - % roots infected | 146475.78 | 1 | 146475.78 | | |
| A - area infected | 64530.28 | 1 | 64530.28 | | |
| N BY I | 9905.28 | 1 | 9905.28 | | |
| N BY R | 24035.28 | 1 | 24035.28 | | |
| N BY P | 14492.53 | 1 | 14492.53 | | |
| N BY A | 223613.28 | 1 | 223613.28 | | |
| I BY R | 9556.53 | 1 | 9556.53 | | |
| I BY P | 2719.53 | 1 | 2719.53 | | |
| I BY A | 26049.03 | 1 | 26049.03 | | |
| R BY P | 1092.78 | 1 | 1092.78 | | |
| R BY A | 16425.78 | 1 | 16425.78 | | |
| P BY A | 140.28 | 1 | 140.28 | | |
| N BY I BY R | 101.53 | 1 | 101.53 | | |
| N BY I BY P | 2363.28 | 1 | 2363.28 | | |
| N BY I BY A | 2574.03 | 1 | 2574.03 | | |
| N BY R BY P | 1471.53 | 1 | 1471.53 | | |
| N BY R BY A | 1498.78 | 1 | 1498.78 | | |
| N BY P BY A | 9765.03 | 1 | 9765.03 | | |
| I BY R BY P | 59254.03 | 1 | 59254.03 | | |
| I BY R BY A | 442.53 | 1 | 442.53 | | |
| I BY P BY A | 6022.53 | 1 | 6022.53 | | |
| R BY P BY A | 3341.53 | 1 | 3341.53 | | |
| N BY I BY R BY P | 7595.28 | 1 | 7595.28 | | |
| N BY I BY R BY A | 520.03 | 1 | 520.03 | | |
| N BY I BY P BY A | 23490.28 | 1 | 23490.28 | | |
| N BY R BY P BY A | 60813.28 | 1 | 60813.28 | | |
| I BY R BY P BY A | 12051.28 | 1 | 12051.28 | | |
| N BY I BY R BY P BY A | 7906.53 | 1 | 7906.53 | | |

Table 6.—Analysis of variance for tree mortality rate in second cycle, 2003, for *Armillaria* in stand 4019.

| Source of variation | SS | DF | MS | F | Sig of F |
|-----------------------|------------|----|------------|---|----------|
| Residual | .00 | 0 | | | |
| Constant | 5658248.00 | 1 | 5658248.00 | | |
| N - centers | 246402.00 | 1 | 246402.00 | | |
| I - % trees infected | 820.12 | 1 | 820.12 | | |
| R - random start | 12.50 | 1 | 12.50 | | |
| P - % roots infected | 154568.00 | 1 | 154568.00 | | |
| A - area infected | 95484.50 | 1 | 95484.50 | | |
| N BY I | 7381.13 | 1 | 7381.13 | | |
| N BY R | 9522.00 | 1 | 9522.00 | | |
| N BY P | 28800.00 | 1 | 28800.00 | | |
| N BY A | 210600.50 | 1 | 210600.50 | | |
| I BY R | 8385.12 | 1 | 8385.12 | | |
| I BY P | 2346.12 | 1 | 2346.12 | | |
| I BY A | 47895.12 | 1 | 47895.12 | | |
| R BY P | 7812.50 | 1 | 7812.50 | | |
| R BY A | 15664.50 | 1 | 15664.50 | | |
| P BY A | 50.00 | 1 | 50.00 | | |
| N BY I BY R | 2016.12 | 1 | 2016.12 | | |
| N BY I BY P | 66.13 | 1 | 66.13 | | |
| N BY I BY A | 1830.12 | 1 | 1830.12 | | |
| N BY R BY P | 1250.00 | 1 | 1250.00 | | |
| N BY R BY A | 8712.00 | 1 | 8712.00 | | |
| N BY P BY A | 1682.00 | 1 | 1682.00 | | |
| I BY R BY P | 37128.13 | 1 | 37128.13 | | |
| I BY R BY A | 1596.12 | 1 | 1596.12 | | |
| I BY P BY A | 4656.13 | 1 | 4656.13 | | |
| R BY P BY A | 11552.00 | 1 | 11552.00 | | |
| N BY I BY R BY P | 5778.12 | 1 | 5778.12 | | |
| N BY I BY R BY A | 1225.13 | 1 | 1225.13 | | |
| N BY I BY P BY A | 11026.12 | 1 | 11026.12 | | |
| N BY R BY P BY A | 66612.50 | 1 | 66612.50 | | |
| I BY R BY P BY A | 2850.12 | 1 | 2850.12 | | |
| N BY I BY R BY P BY A | 8385.12 | 1 | 8385.12 | | |

Table 8.—Summary of significance levels from analyses of variance for tree mortality in *Armillaria*-infected stands. Significance levels are for 10-year simulation cycles that end in the years given below.

| Source | Year | | | | | |
|-----------------------|------|------|------|------|------|------|
| | 1993 | 2003 | 2013 | 2023 | 2033 | 2083 |
| N - centers | .074 | .000 | .000 | .000 | .000 | .000 |
| I - % trees infected | .000 | .424 | .000 | .005 | .324 | .140 |
| R - random start | .546 | .143 | .665 | .180 | .734 | .329 |
| P - % roots infected | .000 | .000 | .325 | .852 | .963 | .621 |
| A - area infected | .313 | .000 | .000 | .001 | .000 | .037 |
| N BY I | .248 | .677 | .551 | .616 | .761 | .655 |
| N BY R | .053 | .598 | .880 | .210 | .022 | .000 |
| N BY P | .526 | .414 | .105 | .621 | .174 | .523 |
| N BY A | .537 | .000 | .527 | .090 | .885 | .433 |
| I BY R | .617 | .976 | .416 | .833 | .396 | .800 |
| I BY P | .558 | .600 | .184 | .590 | .737 | .763 |
| I BY A | .941 | .030 | .253 | .737 | .903 | .160 |
| R BY P | .839 | .153 | .683 | .163 | .636 | .875 |
| R BY A | .196 | .978 | .280 | .660 | .640 | .638 |
| P BY A | .880 | .331 | .468 | .342 | .544 | .856 |
| N BY I BY R | .837 | .910 | .623 | .726 | .662 | .604 |
| N BY I BY P | .988 | .929 | .520 | .951 | .724 | .243 |
| N BY I BY A | .542 | .178 | .917 | .180 | .747 | .781 |
| N BY R BY P | .235 | .058 | .273 | .599 | .487 | .182 |
| N BY R BY A | .986 | .756 | .082 | .428 | .771 | .122 |
| N BY P BY A | .805 | .384 | .691 | .520 | .087 | .392 |
| I BY R BY P | .987 | .173 | .669 | .768 | .140 | .448 |
| I BY R BY A | .555 | .045 | .425 | .291 | .396 | .492 |
| I BY P BY A | .725 | .897 | .636 | .935 | .636 | .318 |
| R BY P BY A | .838 | .097 | .305 | .449 | .381 | .763 |
| N BY I BY R BY P | .779 | .097 | .887 | .453 | .636 | .708 |
| N BY I BY R BY A | .404 | .777 | .445 | .453 | .605 | .274 |
| N BY I BY P BY A | .721 | .019 | .711 | .369 | .208 | .763 |
| N BY R BY P BY A | .955 | .154 | .411 | .774 | .714 | .122 |
| I BY R BY P BY A | .612 | .625 | .729 | .559 | .493 | .341 |
| N BY I BY R BY P BY A | .844 | .870 | .148 | .941 | .487 | .726 |

Table 9.—Summary of significance levels from analyses of variance for disease area in *Armillaria*-infected stands. Significance levels are for 10-year simulation cycles that end in the years given below.

| Source/ | Year | | | | | |
|-----------------------|-------|------|------|------|------|------|
| | 1993 | 2003 | 2013 | 2023 | 2033 | 2083 |
| N - centers | .000 | .000 | .000 | .000 | .000 | .000 |
| I - % trees infected | 1.000 | .708 | .466 | .885 | .930 | .318 |
| R - random start | .126 | .006 | .019 | .180 | .099 | .003 |
| P - % roots infected | 1.000 | .898 | .831 | .414 | .155 | .053 |
| A - area infected | .000 | .000 | .000 | .000 | .000 | .000 |
| N BY I | 1.000 | .446 | .639 | .977 | .813 | .694 |
| N BY R | .049 | .003 | .002 | .002 | .000 | .000 |
| N BY P | 1.000 | .734 | .681 | .930 | .483 | .806 |
| N BY A | .472 | .001 | .002 | .003 | .034 | .373 |
| I BY R | 1.000 | .138 | .471 | .500 | .334 | .984 |
| I BY P | 1.000 | .858 | .798 | .999 | .577 | .809 |
| I BY A | .226 | .334 | .031 | .000 | .002 | .362 |
| R BY P | 1.000 | .715 | .695 | .559 | .925 | .826 |
| R BY A | .503 | .854 | .692 | .473 | .340 | .268 |
| P BY A | .226 | .370 | .307 | .901 | .989 | .965 |
| N BY I BY R | 1.000 | .130 | .379 | .348 | .261 | .747 |
| N BY I BY P | 1.000 | .772 | .343 | .329 | .674 | .199 |
| N BY I BY A | .226 | .029 | .040 | .000 | .004 | .067 |
| N BY R BY P | 1.000 | .918 | .709 | .203 | .399 | .151 |
| N BY R BY A | .016 | .098 | .159 | .187 | .130 | .273 |
| N BY P BY A | .226 | .276 | .527 | .397 | .201 | .307 |
| I BY R BY P | 1.000 | .753 | .525 | .688 | .283 | .376 |
| I BY R BY A | .226 | .019 | .075 | .326 | .090 | .036 |
| I BY P BY A | .226 | .322 | .263 | .626 | .525 | .531 |
| R BY P BY A | .226 | .287 | .510 | .432 | .179 | .166 |
| N BY I BY R BY P | 1.000 | .878 | .819 | .932 | .623 | .981 |
| N BY I BY R BY A | .226 | .339 | .307 | .159 | .648 | .520 |
| N BY I BY P BY A | .226 | .426 | .390 | .295 | .515 | .758 |
| I BY R BY P BY A | .226 | .384 | .892 | .830 | .225 | .793 |
| N BY R BY P BY A | .226 | .412 | .100 | .494 | .518 | .277 |
| N BY I BY R BY P BY A | .226 | .310 | .709 | .584 | .706 | .791 |

Table 10.—Summary of significance levels from analyses of covariance for merchantable volume in disease area of *Armillaria*-infected stands. Significance levels are for 10-year simulation cycles that end in the years given below.

| Source | Year | | | | | |
|-----------------------|------|------|------|------|------|------|
| | 1993 | 2003 | 2013 | 2023 | 2033 | 2083 |
| Covariant | .000 | .000 | .000 | .000 | .000 | .000 |
| N - centers | .000 | .291 | .000 | .000 | .000 | .000 |
| I - % trees infected | .000 | .000 | .000 | .000 | .000 | .188 |
| R - random start | .466 | .745 | .005 | .009 | .659 | .934 |
| P - % roots infected | .000 | .803 | .507 | .258 | .113 | .258 |
| A - area infected | .109 | .135 | .000 | .000 | .000 | .001 |
| N BY I | .000 | .000 | .000 | .151 | .096 | .779 |
| N BY R | .698 | .314 | .088 | .458 | .029 | .001 |
| N BY P | .831 | .986 | .281 | .282 | .133 | .414 |
| N BY A | .010 | .000 | .000 | .026 | .144 | .504 |
| I BY R | .132 | .054 | .030 | .348 | .504 | .738 |
| I BY P | .000 | .282 | .274 | .439 | .625 | .239 |
| I BY A | .347 | .034 | .929 | .704 | .153 | .156 |
| R BY P | .580 | .807 | .103 | .038 | .804 | .964 |
| R BY A | .201 | .675 | .028 | .280 | .472 | .141 |
| P BY A | .292 | .811 | .623 | .147 | .874 | .675 |
| N BY I BY R | .094 | .003 | .942 | .791 | .589 | .134 |
| N BY I BY P | .655 | .875 | .943 | .605 | .309 | .683 |
| N BY I BY A | .178 | .405 | .356 | .004 | .717 | .345 |
| N BY R BY P | .597 | .788 | .798 | .629 | .354 | .128 |
| N BY R BY A | .005 | .000 | .018 | .334 | .882 | .755 |
| N BY P BY A | .435 | .889 | .317 | .588 | .392 | .225 |
| I BY R BY P | .628 | .666 | .772 | .300 | .397 | .426 |
| I BY R BY A | .061 | .001 | .322 | .031 | .457 | .197 |
| I BY P BY A | .740 | .885 | .083 | .955 | .473 | .039 |
| R BY P BY A | .723 | .660 | .052 | .666 | .948 | .861 |
| N BY I BY R BY P | .845 | .595 | .303 | .089 | .104 | .976 |
| N BY I BY R BY A | .001 | .066 | .200 | .826 | .184 | .409 |
| N BY I BY P BY A | .710 | .935 | .109 | .410 | .710 | .322 |
| I BY R BY P BY A | .530 | .492 | .001 | .239 | .040 | .018 |
| N BY R BY P BY A | .341 | .813 | .000 | .724 | .359 | .009 |
| N BY I BY R BY P BY A | .540 | .872 | .174 | .317 | .961 | .336 |

Table 11.—Summary of significance levels from analyses of variance for tree mortality in *Phellinus*-infected stands. Significance levels are for 10-year simulation cycles that end in the years given below.

| Source | Year | | | | | |
|-----------------------|------|------|------|------|------|------|
| | 1993 | 2003 | 2013 | 2023 | 2033 | 2083 |
| N - centers | .165 | .163 | .132 | .110 | .017 | .135 |
| I - % trees infected | .001 | .680 | .183 | .334 | .445 | .494 |
| R - random start | .613 | .581 | .786 | .805 | .811 | .475 |
| P - % roots infected | .140 | .087 | .363 | .985 | .774 | .894 |
| A - area infected | .639 | .560 | .176 | .160 | .248 | .465 |
| N BY I | .537 | .645 | .816 | .733 | .919 | .631 |
| N BY R | .905 | .532 | .908 | .325 | .447 | .269 |
| N BY P | .966 | .991 | .794 | .849 | .703 | .919 |
| N BY A | .755 | .778 | .926 | .527 | .997 | .484 |
| I BY R | .931 | .746 | .973 | .889 | .936 | .919 |
| I BY P | .927 | .968 | .890 | .466 | .656 | .631 |
| I BY A | .795 | .818 | .911 | .821 | .843 | .881 |
| R BY P | .975 | .539 | .921 | .953 | .833 | .931 |
| R BY A | .627 | .730 | .437 | .484 | .969 | .944 |
| P BY A | .831 | .815 | .857 | .626 | .779 | .631 |
| N BY I BY R | .882 | .648 | .827 | .883 | .902 | .759 |
| N BY I BY P | .935 | .949 | .997 | .791 | .611 | .771 |
| N BY I BY A | .927 | .896 | .809 | .663 | .613 | .587 |
| N BY R BY P | .843 | .786 | .777 | .957 | .509 | .956 |
| N BY R BY A | .648 | .946 | .996 | .451 | .420 | .735 |
| N BY P BY A | .940 | .953 | .888 | .890 | .792 | .981 |
| I BY R BY P | .978 | .769 | .758 | .545 | .556 | .894 |
| I BY R BY A | .926 | .838 | .418 | .836 | .883 | .944 |
| I BY P BY A | .958 | .735 | .967 | .819 | .799 | .700 |
| R BY P BY A | .999 | .713 | .973 | .849 | .819 | .759 |
| N BY I BY R BY P | .925 | .631 | .934 | .870 | .503 | .944 |
| N BY I BY R BY A | .968 | .900 | .859 | .660 | .872 | .844 |
| N BY I BY P BY A | .973 | .865 | .744 | .857 | .947 | .981 |
| I BY R BY P BY A | .957 | .915 | .723 | .795 | .464 | .906 |
| N BY R BY P BY A | .976 | .762 | .630 | .912 | .755 | .832 |
| N BY I BY R BY P BY A | .955 | .987 | .663 | .337 | .644 | .894 |

Table 12.—Summary of significance levels from analyses of variance for disease area in *Phellinus*-infected stands. Significance levels are for 10-year simulation cycles that end in the years given below.

| Source | Year | | | | | |
|-----------------------|-------|------|------|------|------|------|
| | 1993 | 2003 | 2013 | 2023 | 2033 | 2083 |
| N - centers | .000 | .000 | .000 | .000 | .000 | .000 |
| I - % trees infected | 1.000 | .710 | .685 | .746 | .830 | .695 |
| R - random start | .852 | .318 | .257 | .221 | .076 | .473 |
| P - % roots infected | 1.000 | .849 | .778 | .763 | .716 | .776 |
| A - area infected | .000 | .000 | .000 | .000 | .000 | .000 |
| N BY I | 1.000 | .471 | .602 | .635 | .577 | .153 |
| N BY R | .022 | .002 | .001 | .000 | .000 | .000 |
| N BY P | 1.000 | .780 | .956 | .861 | .662 | .726 |
| N BY A | .035 | .010 | .022 | .039 | .266 | .061 |
| I BY R | 1.000 | .815 | .829 | .822 | .691 | .787 |
| I BY P | 1.000 | .950 | .716 | .816 | .544 | .912 |
| I BY A | 1.000 | .855 | .796 | .982 | .891 | .694 |
| R BY P | 1.000 | .715 | .960 | .832 | .828 | .729 |
| R BY A | .903 | .727 | .329 | .570 | .868 | .155 |
| P BY A | 1.000 | .893 | .820 | .607 | .897 | .933 |
| N BY I BY R | 1.000 | .997 | .942 | .952 | .590 | .684 |
| N BY I BY P | 1.000 | .979 | .644 | .936 | .582 | .933 |
| N BY I BY A | 1.000 | .455 | .635 | .601 | .927 | .995 |
| N BY R BY P | 1.000 | .766 | .891 | .982 | .888 | .782 |
| N BY R BY A | .016 | .011 | .011 | .053 | .368 | .969 |
| N BY P BY A | 1.000 | .858 | .676 | .416 | .954 | .715 |
| I BY R BY P | 1.000 | .953 | .904 | .645 | .886 | .776 |
| I BY R BY A | 1.000 | .562 | .326 | .322 | .502 | .511 |
| I BY P BY A | 1.000 | .864 | .804 | .937 | .921 | .888 |
| R BY P BY A | 1.000 | .997 | .824 | .527 | .620 | .631 |
| N BY I BY R BY P | 1.000 | .964 | .776 | .340 | .767 | .394 |
| N BY I BY R BY A | 1.000 | .476 | .339 | .370 | .731 | .887 |
| N BY I BY P BY A | 1.000 | .941 | .785 | .664 | .767 | .641 |
| I BY R BY P BY A | 1.000 | .908 | .676 | .554 | .803 | .891 |
| N BY R BY P BY A | 1.000 | .803 | .757 | .609 | .816 | .883 |
| N BY I BY R BY P BY A | 1.000 | .849 | .981 | .964 | .393 | .799 |

Table 13.—Summary of significance levels from analyses of covariance for merchantable volume in disease area of *Phellinus*-infected stands. Significance levels are for 10-year simulation cycles that end in the years given below.

| Source | Year | | | | | |
|-----------------------|------|------|------|------|------|------|
| | 1993 | 2003 | 2013 | 2023 | 2033 | 2083 |
| Covariant | .000 | .000 | .000 | .000 | .000 | .000 |
| N - centers | .117 | .013 | .000 | .000 | .000 | .731 |
| I - % trees infected | .000 | .000 | .000 | .000 | .047 | .408 |
| R - random start | .889 | .390 | .375 | .901 | .985 | .269 |
| P - % roots infected | .000 | .000 | .265 | .305 | .920 | .849 |
| A - area infected | .749 | .009 | .000 | .000 | .024 | .024 |
| N BY I | .506 | .262 | .028 | .129 | .848 | .966 |
| N BY R | .808 | .933 | .534 | .325 | .211 | .417 |
| N BY P | .594 | .582 | .604 | .810 | .851 | .800 |
| N BY A | .880 | .986 | .731 | .954 | .792 | .418 |
| I BY R | .915 | .989 | .847 | .932 | .710 | .727 |
| I BY P | .004 | .341 | .580 | .838 | .691 | .807 |
| I BY A | .619 | .197 | .108 | .628 | .802 | .791 |
| R BY P | .946 | .895 | .899 | .716 | .828 | .876 |
| R BY A | .980 | .877 | .629 | .927 | .721 | .803 |
| P BY A | .586 | .899 | .735 | .851 | .641 | .762 |
| N BY I BY R | .849 | .756 | .478 | .692 | .902 | .870 |
| N BY I BY P | .735 | .835 | .902 | .985 | .988 | .715 |
| N BY I BY A | .949 | .569 | .891 | .955 | .711 | .843 |
| N BY R BY P | .886 | .752 | .971 | .944 | .869 | .928 |
| N BY R BY A | .928 | .736 | .995 | .587 | .522 | .843 |
| N BY P BY A | .930 | .841 | .477 | .399 | .995 | .648 |
| I BY R BY P | .902 | .955 | .861 | .629 | .860 | .828 |
| I BY R BY A | .996 | .820 | .536 | .713 | .863 | .839 |
| I BY P BY A | .824 | .964 | .789 | .894 | .822 | .938 |
| R BY P BY A | .988 | .986 | .915 | .675 | .941 | .896 |
| N BY I BY R BY P | .895 | .978 | .642 | .372 | .882 | .731 |
| N BY I BY R BY A | .972 | .712 | .506 | .871 | .748 | .739 |
| N BY I BY P BY A | .982 | .892 | .946 | .781 | .871 | .677 |
| I BY R BY P BY A | .988 | .925 | .839 | .798 | .683 | .985 |
| N BY R BY P BY A | .999 | .891 | .644 | .920 | .950 | .934 |
| N BY I BY R BY P BY A | .966 | .988 | .675 | .693 | .748 | .949 |

Table 15.—Summary of significance levels from analyses of variance for infected tree density by stand age for *Armillaria*-infected stands following harvest.

| Source | Stand Age | | | | |
|-----------------------|-----------|------|------|------|------|
| | 30 | 40 | 50 | 60 | 70 |
| L - larch planted | .209 | .388 | .920 | .357 | .457 |
| I - % trees infected | .529 | .437 | .271 | .143 | .277 |
| R - random start | .529 | .795 | .431 | .812 | .947 |
| S - stumps removed | .013 | .001 | .000 | .000 | .000 |
| J - jump in infection | .529 | .863 | .616 | .582 | .801 |
| L BY I | .061 | .863 | .414 | .976 | .577 |
| L BY R | .529 | .605 | .785 | .710 | .926 |
| L BY S | .209 | .863 | .989 | .964 | .595 |
| L BY J | .529 | .795 | .763 | .835 | .642 |
| I BY R | 1.000 | .262 | .875 | .476 | .532 |
| I BY S | .529 | .666 | .920 | .882 | .301 |
| I BY J | 1.000 | .729 | .398 | .306 | .680 |
| R BY S | .529 | .795 | .556 | .603 | .863 |
| R BY J | 1.000 | .863 | .966 | .699 | .710 |
| S BY J | .529 | .729 | .720 | .327 | .989 |
| L BY I BY R | 1.000 | .490 | .875 | .941 | .989 |
| L BY I BY S | .061 | .388 | .537 | .320 | .410 |
| L BY I BY J | 1.000 | .931 | .920 | .458 | .905 |
| L BY R BY S | .529 | .490 | .785 | .882 | .604 |
| L BY R BY J | .209 | .666 | .920 | .624 | .541 |
| L BY S BY J | .529 | .931 | .500 | .688 | .449 |
| I BY R BY S | 1.000 | .262 | .636 | .710 | .720 |
| I BY R BY J | .529 | .604 | .398 | .882 | .671 |
| I BY S BY J | 1.000 | .604 | .382 | .552 | .821 |
| R BY S BY J | 1.000 | .863 | .989 | .365 | .936 |
| L BY I BY R BY S | 1.000 | .388 | .556 | .766 | .740 |
| L BY I BY R BY J | .529 | .437 | .943 | .666 | .490 |
| L BY I BY S BY J | 1.000 | .795 | .556 | .542 | .680 |
| L BY R BY S BY J | .209 | .795 | .875 | .929 | .790 |
| I BY R BY S BY J | .529 | .604 | .323 | .710 | .936 |
| L BY I BY R BY S BY J | .529 | .545 | .943 | .286 | .730 |

Table 14.—Keywords for Prognosis and Western Root Disease Models with carryover submodel.

| | | | | | | | | |
|---|--|-----|-------|-----|-----|----|---|---|
| NUMCYCLE | 10 | | | | | | | |
| INVYEAR | 1983 | | | | | | | |
| COMMENT | PROGNOSIS VERSION NUMBER 15 WAS SELECTED | | | | | | | |
| SCALE | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| END | | | | | | | | |
| TIMEINT | | 2 | 5 | | | | | |
| TIMEINT | | 3 | 5 | | | | | |
| TIMEINT | | 4 | 5 | | | | | |
| TIMEINT | | 5 | 5 | | | | | |
| THINDBH | 1993. | .1 | 99. | 1. | | | | |
| ESTAB | 1994. | | | | | | | |
| BURNPREP | 1995. | 95. | | | | | | |
| TALLYONE | 1998. | | | | | | | |
| TALLYTWO | 2008. | | | | | | | |
| RESETAGE | 1998. | 5. | | | | | | |
| PLANT | 1996. | 2. | 000. | 80. | | | | |
| END | | | | | | | | |
| RRIN | | | | | | | | |
| RRTYPE | 1 | | | | | | | |
| SPREAD | 1 | | | | | | | |
| RRINIT | 0 | 1 | 1 | 19 | .40 | 4 | | |
| SAREA | 23 | | | | | | | |
| RSEED | 3941. | | | | | | | |
| CARRY | 1 | 4 | .00 | | | | | |
| PSTUMP | 1994. | .01 | 5.0 | | | | | |
| RRJUMP | 1 | | | | | | | |
| RRECHO | | | | | | | | |
| END | | | | | | | | |
| ECHOSUM | | | | | | | | |
| STDIDENT | | | | | | | | |
| CROW CREEK STAND 2025 | | | | | | | | |
| DESIGN | 40 | 300 | 5.000 | 7 | 0 | 1 | | |
| STDINFO | 116 | 530 | 130 | 45 | 10 | 33 | | |
| GROWTH | 0 | 5 | | | | | | |
| TREEFMT | | | | | | | | |
| (13X,I4,T18,I4,T28,F2.0,T30,I1,T33,A2,F3.1,F2.1,3X,F3.0,T43,F3.0,T54,F2.0,T46,I1,T48,3(I2,I1),T22,I1,T22,I1,T63,I2,I3,I3,I1,I1) | | | | | | | | |
| PROCESS | | | | | | | | |
| STOP | | | | | | | | |

Table 16.—Summary of significance levels from analyses of variance for infected area by stand age for *Armillaria*-infected stands following harvest.

| Source | Stand Age | | | | |
|-----------------------|-----------|------|------|------|------|
| | 30 | 40 | 50 | 60 | 70 |
| L - larch planted | .856 | .897 | .829 | .705 | .727 |
| I - % trees infected | .004 | .005 | .005 | .010 | .009 |
| R - random start | .988 | .945 | .997 | .888 | .911 |
| S - stumps removed | .000 | .000 | .000 | .000 | .000 |
| J - jump in infection | .730 | .805 | .838 | .770 | .781 |
| L BY I | .477 | .505 | .505 | .595 | .580 |
| L BY R | .808 | .822 | .826 | .776 | .747 |
| L BY S | .453 | .434 | .504 | .575 | .610 |
| L BY J | .878 | .897 | .944 | .898 | .872 |
| I BY R | .565 | .584 | .632 | .528 | .624 |
| I BY S | .458 | .473 | .609 | .538 | .761 |
| I BY J | .929 | .871 | .906 | .866 | .953 |
| R BY S | .667 | .612 | .679 | .577 | .620 |
| R BY J | .953 | .989 | .928 | .991 | .950 |
| S BY J | .581 | .659 | .690 | .612 | .625 |
| L BY I BY R | .713 | .736 | .768 | .731 | .785 |
| L BY I BY S | .587 | .584 | .614 | .511 | .580 |
| L BY I BY J | .845 | .863 | .857 | .898 | .909 |
| L BY R BY S | .995 | .992 | .964 | .914 | .838 |
| L BY R BY J | .808 | .849 | .793 | .815 | .828 |
| L BY S BY J | .882 | .883 | .905 | .839 | .782 |
| I BY R BY S | .469 | .464 | .467 | .608 | .589 |
| I BY R BY J | .995 | .984 | .991 | .984 | .993 |
| I BY S BY J | .904 | .848 | .889 | .881 | .988 |
| R BY S BY J | .999 | .973 | .967 | .973 | .991 |
| L BY I BY R BY S | .838 | .841 | .868 | .921 | .924 |
| L BY I BY R BY J | .741 | .762 | .692 | .738 | .728 |
| L BY I BY S BY J | .895 | .902 | .955 | .950 | .999 |
| L BY R BY S BY J | .804 | .856 | .818 | .888 | .928 |
| I BY R BY S BY J | .862 | .875 | .858 | .843 | .803 |
| L BY I BY R BY S BY J | .990 | .985 | .939 | .981 | .992 |

Table 17.—Analysis of variance for frequency of new centers for stand age 30 in *Armillaria*-infected stands following harvest.

| Source of variation | SS | DF | MS | F | Sig of F |
|-----------------------|----------|----|----------|-------|----------|
| Within cells | 33725.50 | 96 | 351.31 | | |
| Constant | 20000.00 | 1 | 20000.00 | 56.93 | .000 |
| L - larch planted | 7.03 | 1 | 7.03 | .02 | .888 |
| I - % trees infected | 1682.00 | 1 | 1682.00 | 4.79 | .031 |
| R - random start | 1.12 | 1 | 1.12 | .00 | .955 |
| S - stumps removed | 18192.78 | 1 | 18192.78 | 51.79 | .000 |
| J - jump in infection | .03 | 1 | .03 | .00 | .992 |
| L BY I | 7.03 | 1 | 7.03 | .02 | .888 |
| L BY R | 1.53 | 1 | 1.53 | .00 | .947 |
| L BY S | 15.12 | 1 | 15.12 | .04 | .836 |
| L BY J | 12.50 | 1 | 12.50 | .04 | .851 |
| I BY R | 3.12 | 1 | 3.12 | .01 | .925 |
| I BY S | 1262.53 | 1 | 1262.53 | 3.59 | .061 |
| I BY J | 26.28 | 1 | 26.28 | .07 | .785 |
| R BY S | 3.78 | 1 | 3.78 | .01 | .918 |
| R BY J | 1.53 | 1 | 1.53 | .00 | .947 |
| S BY J | .50 | 1 | .50 | .00 | .970 |
| L BY I BY R | 5.28 | 1 | 5.28 | .02 | .903 |
| L BY I BY S | 1.12 | 1 | 1.12 | .00 | .955 |
| L BY I BY J | .12 | 1 | .12 | .00 | .985 |
| L BY R BY S | .12 | 1 | .12 | .00 | .985 |
| L BY R BY J | 60.50 | 1 | 60.50 | .17 | .679 |
| L BY S BY J | 11.28 | 1 | 11.28 | .03 | .858 |
| I BY R BY S | 13.78 | 1 | 13.78 | .04 | .843 |
| I BY R BY J | .03 | 1 | .03 | .00 | .992 |
| I BY S BY J | 21.13 | 1 | 21.13 | .06 | .807 |
| R BY S BY J | 1.12 | 1 | 1.12 | .00 | .955 |
| L BY I BY R BY S | 1.12 | 1 | 1.12 | .00 | .955 |
| L BY I BY R BY J | 36.12 | 1 | 36.12 | .10 | .749 |
| L BY I BY S BY J | .03 | 1 | .03 | .00 | .992 |
| L BY R BY S BY J | 63.28 | 1 | 63.28 | .18 | .672 |
| I BY R BY S BY J | .50 | 1 | .50 | .00 | .970 |
| L BY I BY R BY S BY J | 34.03 | 1 | 34.03 | .10 | .756 |

Table 19.—Summary of significance levels from analyses of variance for infected area by stand age in *Phellinus*-infected stands following harvest.

| Source | 30 | 40 | Stand Age 50 | 60 | 70 |
|----------------------|------|------|-----------------|------|------|
| L - larch planted | .000 | .000 | .000 | .000 | .001 |
| I - % trees infected | .106 | .075 | .141 | .117 | .126 |
| R - random start | .589 | .365 | .400 | .363 | .351 |
| S - stumps removed | .106 | .122 | .150 | .132 | .112 |
| L BY I | .752 | .793 | .963 | .814 | .742 |
| L BY R | .898 | .640 | .684 | .802 | .886 |
| L BY S | .767 | .768 | .767 | .605 | .539 |
| I BY R | .915 | .695 | .771 | .991 | .987 |
| I BY S | .854 | .947 | .915 | .976 | .965 |
| R BY S | .963 | .950 | .971 | .933 | .941 |
| L BY I BY R | .911 | .929 | .969 | .885 | .997 |
| L BY I BY S | .915 | .857 | .921 | .908 | .990 |
| L BY R BY S | .935 | .885 | .889 | .856 | .944 |
| I BY R BY S | .984 | .997 | .826 | .894 | .923 |
| L BY I BY R BY S | .850 | .770 | .881 | .999 | .878 |

Table 18.—Summary of significance levels from analyses of variance for infected tree density by stand age in *Phellinus*-infected stands following harvest.

| Source | 30 | 40 | Stand Age 50 | 60 | 70 |
|----------------------|-------|------|-----------------|-------|------|
| L - larch planted | .005 | .673 | .192 | .305 | .574 |
| I - % trees infected | .007 | .811 | .941 | .677 | .631 |
| R - random start | 1.000 | .715 | .927 | .880 | .947 |
| S - stumps removed | .196 | .855 | .976 | .954 | .596 |
| L BY I | .416 | .811 | .990 | .917 | .487 |
| L BY R | 1.000 | .800 | .997 | .963 | .330 |
| L BY S | .744 | .789 | .871 | .908 | .330 |
| I BY R | .870 | .989 | .892 | .737 | .667 |
| I BY S | .146 | .933 | .976 | .826 | .529 |
| R BY S | .196 | .877 | .976 | .871 | .804 |
| L BY I BY R | .416 | .922 | .997 | 1.000 | .703 |
| L BY I BY S | .625 | .955 | .997 | .817 | .908 |
| L BY R BY S | .515 | .922 | .948 | .880 | .765 |
| I BY R BY S | .625 | .978 | .941 | .963 | .608 |
| L BY I BY R BY S | .257 | .910 | .983 | .991 | .921 |

Table 20.—Analysis of variance for frequency of new centers for stand age 30 in *Phellinus*-infected stands following harvest.

| Source of variation | SS | DF | MS | F | Sig of F |
|----------------------|-----------|----|-----------|--------|----------|
| Within cells | 52944.75 | 48 | 1103.02 | | |
| Constant | 326755.14 | 1 | 326755.14 | 296.24 | .000 |
| L - larch planted | 12797.27 | 1 | 12797.27 | 11.60 | .001 |
| I - % trees infected | 4607.02 | 1 | 4607.02 | 4.18 | .046 |
| R - random start | 147.02 | 1 | 147.02 | .13 | .717 |
| S - stumps removed | 2562.89 | 1 | 2562.89 | 2.32 | .134 |
| L BY I | 172.27 | 1 | 172.27 | .16 | .694 |
| L BY R | 26.27 | 1 | 26.27 | .02 | .878 |
| L BY S | 141.02 | 1 | 141.02 | .13 | .722 |
| I BY R | 19.14 | 1 | 19.14 | .02 | .896 |
| I BY S | 87.89 | 1 | 87.89 | .08 | .779 |
| R BY S | 15.02 | 1 | 15.02 | .01 | .908 |
| L BY I BY R | 9.77 | 1 | 9.77 | .01 | .925 |
| L BY I BY S | 13.14 | 1 | 13.14 | .01 | .914 |
| L BY R BY S | 15.02 | 1 | 15.02 | .01 | .908 |
| I BY R BY S | 9.77 | 1 | 9.77 | .01 | .925 |
| L BY I BY R BY S | 31.64 | 1 | 31.64 | .03 | .866 |

Literature Cited

- Box, G.E.P.; Hunter, M.G.; Hunter, J.S. 1978. Statistics for experimenters: an introduction to design, data analysis, and model building. New York: John Wiley and Sons. 653 p.
- Ferguson, Dennis E.; Crookston, Nicholas L. 1984. User's guide to the Regeneration Establishment Model—a Prognosis Model extension. Gen. Tech. Rep. INT-161. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 23 p.
- Gnanadesikan, R. 1977. Methods for statistical data analysis of multivariate observations. New York: John Wiley and Sons. 311 p.
- Marsden, M.A. 1992. Sensitivity of the Western Root Disease Model: Inventory of root disease. Res. Pap. RM-303. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station.
- Stage, Albert R.; Shaw, Charles G., III; Marsden, Michael A.; Byler, James W.; Renner, David L.; Eav, Bov B.; McNamee, Peter J.; Sutherland, Glenn D.; Webb, Timothy M. 1990. User's manual for Western Root Disease Model. Gen. Tech. Rep. INT-267. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 49 p.
- Wykoff, William R.; Crookston, Nicholas L.; Stage, Albert R. 1982. Users guide to the Stand Prognosis Model. Gen. Tech. Rep. INT-133. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 112 p.
- Wykoff, William R. 1986. Supplement to the users guide for the Stand Prognosis Model—version 5.0. Gen. Tech. Rep. INT-208. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Research Station. 36 p.

Appendix A

Stand 2025 - Lolo National Forest

| | |
|--------------------------|--|
| Habitat Type: | <i>Thuja plicata</i> / <i>Clintonia uniflora</i> (Western redcedar/Queencup beadlily) |
| Stand age: | over 130 years |
| Aspect: | Northeast |
| Slope: | 10% |
| Elevation: | 3,300 feet |
| Quadratic mean diameter: | 2.3" |
| Largest tree: | 43.90" cedar |
| Inventory trees: | 1 ponderosa pine, 13 Douglas-fir, 25 grand fir, 10 larch, 4 lodgepole pine, 15 cedar, 1 spruce, 1 white pine |
| Trees/acre: | 8,987 total; 65% grand fir, 22% Douglas-fir, 11% cedar, 1% lodgepole pine |
| Volume MCUFT/acre: | 8,340 total; 31% grand fir, 28% larch, 25% cedar, 7% Douglas-fir |

Stand 4019 - Lolo National Forest

| | |
|--------------------------|--|
| Habitat Type: | <i>Thuja plicata</i> / <i>Clintonia uniflora-clintonia uniflora</i> phase (Western redcedar/Queencup beadlily) |
| Stand age: | over 100 years |
| Aspect: | Northeast |
| Slope: | 60% |
| Elevation: | 4,600 feet |
| Quadratic mean diameter: | 3.6" |
| Largest tree: | 27.00" grand fir |
| Inventory trees: | 11 grand fir, 8 cedar, 3 Douglas-fir, 2 spruce |
| Trees/acre: | 2,849 total; 63% grand fir, 30 %cedar, 6%Douglas-fir |
| Volume MCUFT/acre: | 8,104 total; 52% grand fir, 35% cedar, 9% spruce, 4% Douglas-fir |

Stand 4023 - Lolo National Forest

| | |
|--------------------------|--|
| Habitat Type: | <i>Thuja plicata</i> / <i>Clintonia uniflora-Menziesia ferruginea</i> phase (Western redcedar/Queencup beadlily-menziesia phase) |
| Stand age: | over 100 years |
| Aspect: | Northeast |
| Slope: | 70% |
| Elevation: | 4,200 feet |
| Quadratic mean diameter: | 4.7" |
| Largest tree: | 20.60" Douglas-fir |
| Inventory trees: | 25 Douglas-fir, 12 grand fir, 1 lodgepole pine, 12 larch, 1 spruce, 1 cedar |
| Trees/acre: | 1,690 total; 60% Douglas-fir, 29% grand fir, 5% cedar, 3% larch |
| Volume MCUFT/acre: | 5,902 total; 53% Douglas-fir, 36% larch, 8% grand fir, 4% lodgepole pine |

Stand 4040 - Lolo National Forest

| | |
|--------------------------|---|
| Habitat Type: | <i>Thuja plicata</i> / <i>Clintonia uniflora-Aralia nudicaulis</i> phase (Western redcedar/Queencup beadlily-wild sarsaparilla phase) |
| Stand age: | over 70 years |
| Aspect: | Northeast |
| Slope: | 60% |
| Elevation: | 4,000 feet |
| Quadratic mean diameter: | 2.7" |
| Largest tree: | 15.00" grand fir |
| Inventory trees: | 2 cedar, 9 grand fir, 1 lodgepole pine, 3 larch, 7 Douglas-fir, 1 subalpine fir |
| Tree/acre: | 4,926 total; 53% grand fir, 36% Douglas-fir, 5% cedar, 3% larch |
| Volume MCUFT/acre: | 4,476 total; 36% Douglas-fir, 33% grand fir, 18% larch, 13% lodgepole pine |

Marsden, Michael A. 1992. Sensitivity analyses of the Western Root Disease Model to user-specified starting parameters. Res. Pap. RM-306. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station. 20 p.

Tests of the Western Root Disease Model identify the user-supplied parameters to which the model is most sensitive. A series of simulation runs are arranged as a designed experiment. Analysis of variance is used to identify significant starting conditions based on attributes of the stand simulations. Probability plots of the sum of squares associated with the model parameters are used to rank effects. This gives the user a reference for the relative effect of each parameter. Short-term model simulations without the harvest of trees are sensitive to such parameters as the proportion of trees infected and the proportion of root systems colonized. Long-term simulations are more sensitive to such parameters as initial area infected and number of disease centers. Model simulations with harvest are sensitive to the removal of stumps and the planting of resistant species.

Keywords: Simulation, sensitivity analysis, statistics, root disease



Rocky
Mountains



Southwest



Great
Plains

U.S. Department of Agriculture
Forest Service

Rocky Mountain Forest and Range Experiment Station

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